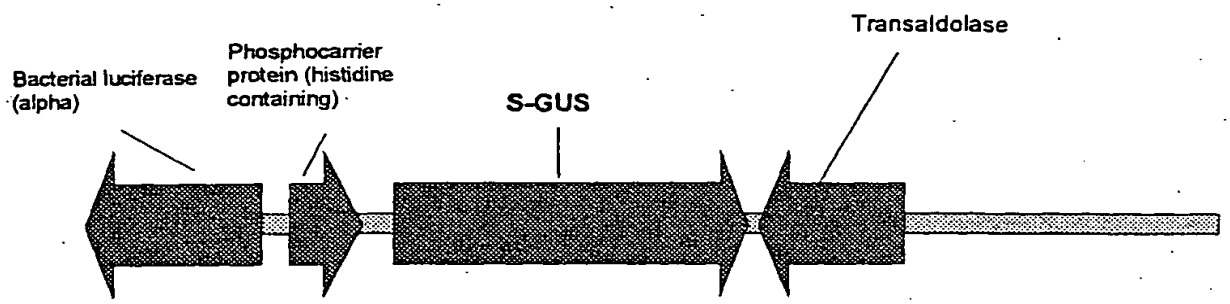
09/936759

Title: MICROBIAL B-GLUCURONIDASE GENES, GENE PRODUCTS AND USES THEREOF
Inventor(s): JEFFERSON ET AL.
DOCKET NO.: 076518-0150

FIGURE 1

```
   1 agcctttact ttttctttcaa cttttcatcc cgatactttt ttgtaatagt ttttttcatt
  61 aataatacaa gtcctgattt tgcaagaata atccttttta gataaaaata tctatgctaa
 121 taataacatg taaccactta catttaaaaa ggagtgctat catgttatat ccaatcaata
 181 cagaaacccg aggagttttt gatttaaatg gggtctggaa ttttaaatta gattacggca
 241 aaggactgga agaaaagtgg tatgaatcaa aactgacaga taccatatca atggctgtac
 301 cttcctccta taatgatatc ggtgttacga aggaaattcg aaaccatatc ggctatgtat
 361 ggtacgagcg tgaatttacc gttcctgctt atttaaaaga tcagcgcatc gtcctgcgtt
 421 ttggttcagc aacacataag gctattgtat acgttaacgg agaactagta gttgaacaca
 481 aaggcggctt cttaccgttt gaggcagaaa taaacaacag cttaagagac ggaatgaatc
 541 gtgtaacagt agcggttgat aatattttag atgattctac gctcccagtt gggctatata
 601 gtgaaagaca tgaagaaggt ttgggaaaag tgattcgtaa taaacctaat tttgacttct
 661 ttaactatgc aggcttacat cgtcctgtaa aaatttatac aacccctttt acctatgttg
 721 aggatatatc ggttgtaacc gattttaacg gtccaacggg aacagttacg tatacagttg
 781 attttcaggg taaggcagaa accgtaaagg ttagtgtagt tgatgaagaa gggaaagttg
 841 ttgcttcaac tgaaggcctc tctggtaatg ttgagattcc taacgttatc ctttgggaac
 901 ctttaaatac ctatctctat caaattaaag ttgagttagt aaatgatggt ctaactattg
 961 atgtatacga agagccattt ggagttcgaa ccgttgaagt aaacgacggg aaattcctca
1021 ttaataacaa accatttttat tttaaagggt tcggaaaaca cgaggatact ccaataaatg
1081 gaagaggctt taatgaagca tcaaatgtaa tggattttaa tattttgaaa tggatcggtg
1141 cgaattcctt tcggacggcg cactatcctt attctgaaga actgatgcgg ctcgcagatc
1201 gtgaagggtt agtcgtcata gatgaaaccc cagcagttgg tgttcatttg aacttttatgg
1261 caacgactgg tttgggcgaa ggttcagaga gagtgagtac ttgggaaaaa atccggacct
1321 ttgaacatca tcaagatgta ctgagagagc tggtttctcg tgataaaaac cacccctctg
1381 ttgtcatgtg gtcgattgca aatgaagcgg ctacggaaga agaaggcgct tatgaatact
1441 ttaagccatt agttgaatta acgaaagaat tagatccaca aaaacgccca gttaccattg
1501 ttttgttcgt aatggcgaca ccagaaacag ataaagtggc ggagttaatt gatgtgattg
1561 cattgaatcg atacaacggc tggtattttg atgggggtga tcttgaagcc gcgaaagtcc
1621 accttcgtca ggaattttcat gcgtggaata aacgctgtcc aggaaaacct ataatgataa
1681 cagagtatgg ggctgatacc gtagctggtt ttcatgatat tgatccggtt atgtttacag
1741 aagagtatca ggttgaatat taccaagcaa atcatgtagt atttgatgaa tttgagaact
1801 ttgttggcga gcaggcctgg aattttgcag actttgctac aagccagggt gtcatgcgtg
1861 ttcaaggtaa caaaaaaggt gttttcacac gcgaccgcaa accaaaatta gcagcacatg
1921 ttttccgcga acgttggaca aacatcccgg atttcggtta taaaaattaa taaaaagctg
1981 gttctccaat aggaggccag ctttttttaca tggatacaat ggttgtaaat taaaaaccct
2041 cttcattttt tatataaaaa tgaagagggt ttttaatttt taaatgttat tacatttttt
```

FIGURE 2



Staphylococcus GUS gene

FIGURE 3A

A

Staphylococcus β-glucuronidase

```
  1  MLYPINTETR GVFDLNGVWN FKLDYGKGLE EKWYESKLTD TISMAVPSSY
 51  NDIGVTKEIR NHIGYVWYER EFTVPAYLKD QRIVLRFGSA THKAIVYVNG
101  ELVVEHKGGF LPFEAEINNS LRDGMNRVTV AVDNILDDST LPVGLYSERH
151  EEGLGKVIRN KPNFDFFNYA GLHRPVKIYT TPFTYVEDIS VVTDFNGPTG
201  TVTYTVDFQG KAETVKVSVV DEEGKVVAST EGLSGNVEIP NVILWEPLNT
251  YLYQIKVELV NDGLTIDVYE EPFGVRTVEV NDGKFLINNK PFYFKGFGKH
301  EDTPINGRGF NEASNVMDFN ILKWIGANSF RTAHYPYSEE LMRLADREGL
351  VVIDETPAVG VHLNFMATTG LGEGSERVST WEKIRTFEHH QDVLRELVSR
401  DKNHPSVVMW SIANEAATEE EGAYEYFKPL VELTKELDPQ KRPVTIVLFV
451  MATPETDKVA ELIDVIALNR YNGWYFDGGD LEAAKVHLRQ EFHAWNKRCP
501  GKPIMITEYG ADTVAGFHDI DPVMFTEEYQ VEYYQANHVV FDEFENFVGE
551  QAWNFADFAT SQGVMRVQGN KKGVFTRDRK PKLAAHVFRE RWTNIPDFGY
601  KN
```

B

Enterobacter/Salmonella ß-glucuronidase

```
  1  GKLSPTPTAY IQDVTVXTDV LENTEQATVL GNVGADGDIR VELRDGQQQI
 51  VAQGLGATGI FELDNPHLWE PGEGYLYELR VTCEANGECD EYPVRVGIRS
101  ITXKGEQFLI NHKPFYLTGF GRHEDADFRG KGFDPVLMVH DHALMNWIGA
151  NSYRTSHYPY AEKMLDWADE HVIVVINETA AGGFNTLSLG ITFDAGERPK
201  ELYSEEAING ETSQQAHLQA IKELIARDKN HPSVVCWSIA NEPDTRPNGA
251  REYFAPLAKA TRELDPTRPI TCVNVMFCDA ESDTITDLFD VVCLNRYYGW
301  YVQSGDLEKA EQMLEQELLA WQSKLHRPII ITEYGVDTLA GMPSVYPDMW
351  SEKYQWKWLE MYHRVFDRGS VC
```

C

Staphylococcus homini ß-D-glucuronidase

```
  1  GLSGNVEIPN VILWEPLNTY LYQIKVELVN DGLTIDVYEE PFGVRTVEVN
 51  DGKFLINNKP FYFKGFGKHE DTPINGRGFN EASNVMDFNI LKWIGANSFR
101  TAHYPYSEEL MRLADREGLV VIDETPAVGV HLNFMATTGL GEGSERVSTW
151  EKIRTFEHHQ DVLRELVSRD KNHPSVVMWS IANEAATEEE GAYEYFKPLG
201  GAAKELDPXK RPVTIVLFVM ATPETDKVAE LIDVIALNRY NGWYFDGGDL
251  EAAKVHLRQE FHAWNKRCPG KPIMITEYGA DTVAGFHDID PVMFTEEYQV
301  EYYQANHVVF DEFENFVGEQ AWNFADFATS QGVMRVQGNK KGVFTRDRKP
351  XLAAHVFRER RTNIPDFGYK NASHHH
```

FIGURE 3B

D

Staphylococcus warneri ß-D-glucuronidase

```
  1  LXLLHPITTG TRGGFALYGX XNLMLDYGXG LTDTWTXSLL TELSRLVVLS
 51  WTTHXLTGEX PAISILWPNS ELTVSXLYXG SLXSSSXLCS SLTXHVVICQ
101  XVTLXVDHTG LIXXFEFMST TCCXXDELVT GTLAXILYHX ILPHGLYRKR
151  HEXGLGKXNF YXLHFAFFXY AXLXRTVXMY XNLVRXQDIX VVTXXHXXXX
201  TVEQCVXXNX KIXSVKITIL DENDHAIXES EGAKGNVTIQ NPILWQPLHA
251  YLYNMKVELL NDNECVDVYT ERFGIRSVEV KDGQFLINDK PFYFKGFGKH
301  EDTYXNGRGL NESANVMDIN LMKWIGANSF RTSHYPYSEE MMRLADEQGI
351  VVIDETTXVG IHLNFMXTLG GSXAHDTWXE FDTLEFHKEV IXDLIXRDKN
401  HAWVVMWXFG NEXGXNKGGA KAXFEPFVNL AGEKDXXXXP VTIVTILXAX
451  RNVCEVXDLV DVVCLXXXXG WYXQSGDLEG AKXALDKEXX EWWKXQXNKP
501  XMFTEYGVDX VVGLXXXPDK MXPEEYKMXF YKGYXKIMDK
```

E

Thermotoga maritima ß-glucuronidase

```
  1  MVRPQRNKKR FILILNGVWN LEVTSKDRPI AVPGSWNEQY QDLCYEEGPF
 51  TYKTTFYVPK XLSQKHIRLY FAAVNTDCEV FLNGEKVGEN HIEYLPFEVD
101  VTGKVKSGEN ELRVVVENRL KVGGFPSKVP DSGTHTVGFF GSFPPANFDF
151  FPYGGIIRPV LIEFTDHARI LDIWVDTSES EPEKKLGKVK VKIEVSEEAV
201  GQEMTIKLGE EEKKIRTSNR FVEGEFILEN ARFWSLEDPY LYPLKVELEK
251  DEYTLDIGIR TISWDEKRLY LNGKPVFLKG FGKHEEFPVL GQGTFYPLMI
301  KDFNLLKWIN ANSFRTSHYP YSEEWLDLAD RLGILVIDEA PHVGITRYHY
351  NPETQKIAED NIRRMIDRHK NHPSVIMWSV ANEPESNHPD AEGFFKALYE
401  TANEMDRTRP VVMVSMMDAP DERTRDVALK YFDIVCVNRY YGWYIYQGRI
451  EEGLQALEKD IEELYARHRK PIFVTEFGAD AIAGIHYDPP QMFSEEYQAE
501  LVEKTIRLLL KKDYIIGTHV WAFADFKTPQ NVRRPILNHK GVFTRDRQPK
551  LVAHVLRRLW SEV
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FIGURE 4A

09/936759

Staphylococcus β-glucuronidase

```
      MetLeuTyrProIleAsnThrGluThrArgGlyValPheAspLeuAsnGl
    1 ATGTTATATCCAATCAATACAGAAACCCGAGGAGTTTTTGATTTAAATGG

      yValTrpAsnPheLysLeuAspTyrGlyLysGlyLeuGluGluLysTrpT
   51 GGTCTGGAATTTTAAATTAGATTACGGCAAAGGACTGGAAGAAAAGTGGT

      yrGluSerLysLeuThrAspThrIleSerMetAlaValProSerSerTyr
  101 ATGAATCAAAACTGACAGATACCATATCAATGGCTGTACCTTCCTCCTAT

      AsnAspIleGlyValThrLysGluIleArgAsnHisIleGlyTyrValTr
  151 AATGATATCGGTGTTACGAAGGAAATTCGAAACCATATCGGCTATGTATG

      pTyrGluArgGluPheThrValProAlaTyrLeuLysAspGlnArgIleV
  201 GTACGAGCGTGAATTTACCGTTCCTGCTTATTTAAAAGATCAGCGCATCG

      alLeuArgPheGlySerAlaThrHisLysAlaIleValTyrValAsnGly
  251 TCCTGCGTTTTGGTTCAGCAACACATAAGGCTATTGTATACGTTAACGGA

      GluLeuValValGluHisLysGlyGlyPheLeuProPheGluAlaGluIl
  301 GAACTAGTAGTTGAACACAAAGGCGGCTTCTTACCGTTTGAGGCAGAAAT

      eAsnAsnSerLeuArgAspGlyMetAsnArgValThrValAlaValAspA
  351 AAACAACAGCTTAAGAGACGGAATGAATCGTGTAACAGTAGCGGTTGATA

      snIleLeuAspAspSerThrLeuProValGlyLeuTyrSerGluArgHis
  401 ATATTTTAGATGATTCTACGCTCCCAGTTGGGCTATATAGTGAAAGACAT

      GluGluGlyLeuGlyLysValIleArgAsnLysProAsnPheAspPhePh
  451 GAAGAAGGTTTGGGAAAAGTGATTCGTAATAAACCTAATTTTGACTTCTT

      eAsnTyrAlaGlyLeuHisArgProValLysIleTyrThrThrProPheT
  501 TAACTATGCAGGCTTACATCGTCCTGTAAAAATTTATACAACCCCTTTTA

      hrTyrValGluAspIleSerValValThrAspPheAsnGlyProThrGly
  551 CCTATGTTGAGGATATATCGGTTGTAACCGATTTTAACGGTCCAACGGGA

      ThrValThrTyrThrValAspPheGlnGlyLysAlaGluThrValLysVa
  601 ACAGTTACGTATACAGTTGATTTTCAGGGTAAGGCAGAAACCGTAAAGGT

      lSerValValAspGluGluGlyLysValValAlaSerThrGluGlyLeuS
  651 TAGTGTAGTTGATGAAGAAGGGAAAGTTGTTGCTTCAACTGAAGGCCTCT
```

FIGURE 4B

```
      erGlyAsnValGluIleProAsnValIleLeuTrpGluProLeuAsnThr
 701  CTGGTAATGTTGAGATTCCTAACGTTATCCTTTGGGAACCTTTAAATACC

      TyrLeuTyrGlnIleLysValGluLeuValAsnAspGlyLeuThrIleAs
 751  TATCTCTATCAAATTAAAGTTGAGTTAGTAAATGATGGTCTAACTATTGA

      pValTyrGluGluProPheGlyValArgThrValGluValAsnAspGlyL
 801  TGTATACGAAGAGCCATTTGGAGTTCGAACCGTTGAAGTAAACGACGGGA

      ysPheLeuIleAsnAsnLysProPheTyrPheLysGlyPheGlyLysHis
 851  AATTCCTCATTAATAACAAACCATTTTATTTTAAAGGGTTCGGAAAACAC

      GluAspThrProIleAsnGlyArgGlyPheAsnGluAlaSerAsnValMe
 901  GAGGATACTCCAATAAATGGAAGAGGCTTTAATGAAGCATCAAATGTAAT

      tAspPheAsnIleLeuLysTrpIleGlyAlaAsnSerPheArgThrAlaH
 951  GGATTTTAATATTTTGAAATGGATCGGTGCGAATTCCTTTCGGACGGCGC

      isTyrProTyrSerGluGluLeuMetArgLeuAlaAspArgGluGlyLeu
1001  ACTATCCTTATTCTGAAGAACTGATGCGGCTCGCAGATCGTGAAGGGTTA

      ValValIleAspGluThrProAlaValGlyValHisLeuAsnPheMetAl
1051  GTCGTCATAGATGAAACCCCAGCAGTTGGTGTTCATTTGAACTTTATGGC

      aThrThrGlyLeuGlyGluGlySerGluArgValSerThrTrpGluLysI
1101  AACGACTGGTTTGGGCGAAGGTTCAGAGAGAGTGAGTACTTGGGAAAAAA

      leArgThrPheGluHisHisGlnAspValLeuArgGluLeuValSerArg
1151  TCCGGACCTTTGAACATCATCAAGATGTACTGAGAGAGCTGGTTTCTCGT

      AspLysAsnHisProSerValValMetTrpSerIleAlaAsnGluAlaAl
1201  GATAAAAACCACCCCTCTGTTGTCATGTGGTCGATTGCAAATGAAGCGGC

      aThrGluGluGluGlyAlaTyrGluTyrPheLysProLeuValGluLeuT
1251  TACGGAAGAAGAAGGCGCTTATGAATACTTTAAGCCATTAGTTGAATTAA

      hrLysGluLeuAspProGlnLysArgProValThrIleValLeuPheVal
1301  CGAAAGAATTAGATCCACAAAAACGCCCAGTTACCATTGTTTTGTTCGTA

      MetAlaThrProGluThrAspLysValAlaGluLeuIleAspValIleAl
1351  ATGGCGACACCAGAAACAGATAAAGTGGCGGAGTTAATTGATGTGATTGC

      aLeuAsnArgTyrAsnGlyTrpTyrPheAspGlyGlyAspLeuGluAlaA
1401  ATTGAATCGATACAACGGCTGGTATTTTGATGGGGGTGATCTTGAAGCCG
```

FIGURE 4C

```
      laLysValHisLeuArgGlnGluPheHisAlaTrpAsnLysArgCysPro
1451  CGAAAGTCCACCTTCGTCAGGAATTTCATGCGTGGAATAAACGCTGTCCA

      GlyLysProIleMetIleThrGluTyrGlyAlaAspThrValAlaGlyPh
1501  GGAAAACCTATAATGATAACAGAGTATGGGGCTGATACCGTAGCTGGTTT

      eHisAspIleAspProValMetPheThrGluGluTyrGlnValGluTyrT
1551  TCATGATATTGATCCGGTTATGTTTACAGAAGAGTATCAGGTTGAATATT

      yrGlnAlaAsnHisValValPheAspGluPheGluAsnPheValGlyGlu
1601  ACCAAGCAAATCATGTAGTATTTGATGAATTTGAGAACTTTGTTGGCGAG

      GlnAlaTrpAsnPheAlaAspPheAlaThrSerGlnGlyValMetArgVa
1651  CAGGCCTGGAATTTTGCAGACTTTGCTACAAGCCAGGGTGTCATGCGTGT

      lGlnGlyAsnLysLysGlyValPheThrArgAspArgLysProLysLeuA
1701  TCAAGGTAACAAAAAAGGTGTTTTCACACGCGACCGCAAACCAAAATTAG

      laAlaHisValPheArgGluArgTrpThrAsnIleProAspPheGlyTyr
1751  CAGCACATGTTTTCCGCGAACGTTGGACAAACATCCCGGATTTCGGTTAT

      LysAsn
1801  AAAAAT
```

FIGURE 4D

***Enterobacter/Salmonella* ß-glucuronidase gene**

CATTGGGGAAACTTTCCCCCACACCTACTGCGTATATTCAGGATGTTACG 50

GTTNTTACTGATGTTTTGGAAAATACTGAACAGGCGACCGTAACTGGGGA 100

ATGTGGGGGCTGATGGTGATATTCGGGTTGAGCTTCGCGATGGGCAGCAA 150

CAAATAGTGGCACAAGGGCTGGGGGCCACAGGTATATTTGAACTGGATAA 200

TCCTCATCTTTGGGAACCAGGTGAAGGGTATTTGTACGAGCTGCGGGTTA 250

CCTGCGAAGCCAATGGTGAGTGTGACGAATATCCAGTACGTGTCGGTATC 300

CGTTCCATTACGGNTAAGGGTGAGCAGTTTTTGATTAACCACAAACCGTT 350

TTATTTAACCCGGTTTTGGTCGACATGAAGATGCAGATTTTCGCGGCAAA 400

GGTTTCGACCCGGGTGTTGATGGTTCACGACCACGCGTTGATGAACTGGA 450

TTGGGCTAACTCCTATCGCACGTCCCACTACCCTTACGCGGAAAAGATGC 500

TCGATTGGGCTGATGAGCACGTATCGTAGTGATTAATGAAACCGCGGCGG 550

GTGGCTTTAACACTTTATCGTTGGGAATCACTTTTGACGCAGGCGAAAGA 600

CCTAAAGAACTTCTACAGCGAAGAGGCGATTAATGGCGAGACTTCAGCAG 650

GCTCACTTGCAGGCTATAAAAGAGCTTATTGCCCGGGATAAAAACCATCC 700

AAGTGTAGTGTGTGGAGTATTGCCAATGAGCCCGACACCCGTCCAAATGG 750

AGCCAGAGAGTACTTTGCGCCTTTAGCTAAGGCCACTCGTGAACTGGATC 800

CGACACGTCCGATTACCTGCGTAAACGTGATGTTCTGCGATGCCGAAAGC 850

GACACCATCACCGACCTGTTCGACGTGGTTTGTCTGAATCGCTATTACGG 900

CTGGTATGTGCAATCAGGTGATTTGGAAAAAGCAGAACAGATGCTGGAGC 950

AAGAACTGCTGGCCTGGCAGTCAAAACTACATCGCCCAATTATTATTACG 1000

GAATACGGTGTCGATACGCTGGCAGGAATGCCCTCGGTTTATCCCGACAT 1050

GTGGAGTGAAAAGTACCAGTGAAATGGCTTGAAATGTATCACCGTGTCTT 1100

TGACCGGGGGAGCGTTTGCAAGCGCNAAGCTTAGTTAACACCGGNGGTAC 1150

CGATCACGCGTNAGGCGCCNCCCATGGNCATATGNGCTAGCNTGCGGCCG 1200

FIGURE 4E

CNATGCATTCTGCAGCGATCGCAGCTGAGTACACGAGCTCACCCGCGGAG 1250

TCGACAAGATCCAAGTACTACCCGGGNATACGTAACTAGTGCATGCTCGC 1300

GAAATATTTAGGCCTTATCGAATTAAT 1328

Pseudomonas ß-D-glucuronidase

CTTGCTGGACNACNGTTNAGGATTTTTAGACACGNGGAGCTAAAGCTTGC 50

TGACCNAACTATCACGCCGGNCGTGCANGCTTGGACCGCGACATTNCCTG 100

ACANGNGAAANACTCCGCCATATCCATCTTTGCTGGCCCAACAGTGAGTT 150

NACNGTNNCGNACNNTNNGANGGATCAGTGNATCGAGCTCCNTTNANNTT 200

CTNCGCTAACATAACATGTNGCATATGTCAATNAATNACGCTGGNCGTGG 250

ANCNCACCGGGCTNATTCGNTGNNATTCGAATTGNATGNCAACAACTNTG 300

NTGCACGNTGGNAAANAATTGCGTNACAGGGACTTTGGCCNCTTCCTAAA 350

CCATNGCATCCTCCCNATGGGCTGTACACGAATGNGCCCCCAAAANGGCN 400

TTCAGAAAGGCAATTTNTAACAAGGCNGANNTTTGACTTTTTCAACTATG 450

CAGNNCTGCACCGGACGCTGAAAATGTACANGACCCTGGGTACGTNCNAC 500

CAAGACATNNAAGTNGTGACCGACTCCATTGTNCTAACCGGGACTGTACC 550

TATAATGCGGACTATCANGGCAATGCATGACGTNGAANCGACACACCAGG 600

ATNAGGAAAACAANTGGTGGNANCNCACCANGCCATGATTGTCACGTTTT 650

GTTAGCNTNGANACNAATTCNATTGCTTTNTTAGCTTNTTANATNAGCCT 700

NTTTANATTAGANTTCTNANTGAGACTGT 730

Salmonella ß-glucuronidase

NCTCATGACCCNCCCNTTTTNGTANCNTNTTTGNNANCTGCTGCANNNGA 50

TCACNACNNGGANNCGGGGNGGGTTCGNNCTCTATGGCNCGNGGAACNNN 100

ATGNTGGNCNACNGTTNANGACTGACAGACACGTGGAGCTAAAGCTTGCT 150

FIGURE 4F


```
GCCGAACTATCACTCAGNTCNTGNAAGTTGGACAACACATTNCCTGACAN  200
GNGAAAAGCCCGCCATATCCATACTGTGCTGGCCCAACANTGAGTTCACN  250
GTCGTCGNACTNTATGANGGATCACCTGTATCGANCTCCNTTNATNTTCT  300
NCAGCTAACATAACTGTGNGCATATGTCAATGNATGACCTGGTCGGTGNA  350
NCACACCGGGCGTNATTGNTGNNATTCGAATTTNATGTCAACAACTTTGN  400
TGCANGNTGGAATGAATCTGGGGGCCAGGGACTTTGGCCANCTTCCTNAA  450
CCATTCGCANCCTCCCCCAGTGGGCTTGTACACNATTGNGCCCCAAAAAG  500
GCNTCAGATAGGCATTTTGACAAGCTCCANNTTAACTTTTTCAACTATGC  550
NGNCCTGCACCGGACGCTGAAAAANGTACANGANCCTTGTACGTTCCACC  600
AAGANATTTAAGGTGTGACCCACNTCCATTTTCCTAACNGGACTGTGACT  650
NATAAAGGNTGACCNTTCANGGACACATTGCAATGACCCTTTNAAACGGA  700
ANAACCCCCGGNTTAAAGGAAAAACAAATTTGGTTGGGNAGTCCANCCAA  750
GGGCCAATTANTTGTTNCNCGGGGGANTAAANCCCCCNCCAATCGATCTT  800
CGAAATTTAAACAGCGCTCCGGCCGCCACGTGCGAATTCCGATATCGGAT  850
GAGGCCAGCGCNAAGCTTAGTTAACACCGGNGGTACCGATCACGCGTNAG  900
GCGCCNCCCATGGNCATATGNGCTAGCNTGCGGCCGCNATGCATTCTGCA  950
GCGATCGCAGCTGAGTACACGAGCTCACCCGCGGAGTCGACAAGATCCAA 1000
GTACTACCCGGGNATACGTAACTAGTGCATGCTCGCGAAATATTTAGGCC 1050
TTATCGAATTAA                                        1063
```

Staphylococcus warneri ß-glucuronidase

```
TANANCTTGTNTCTGCTGCACCCNATCACGACAGGGACCCGGGGNGGGTT   50
CGCGCTCTATGGCNCGNGGAACTTAATGCTGGACTACGGTTNAGGACTGA  100
CAGACACGTGGACTNAAAGCTTGCTGACCGAACTATCACGACTGGTCGTG  150
CTAAGTTGGACCACACATTNCCTGACAGGGGAAANACCCGCCATATCCAT  200
```

FIGURE 4G

CTTGTGGCCCAACAGTGAGTTAACCGTGTCGANCTTATATGANGGATCAC 250

TGNATTCGAGCTCCNTCTTATGTTCTTCGCTAACATANCATGTNGTCATA 300

TGTCAATANGTGACNCTGGNCGTGGATCACACCGGGCTNATTGNTGNATT 350

CGAATTTATGTCAACAACTTGTTGCANGNTGGATGAATTGGTNACAGGGA 400

CTTTGGCCANCATCCTATACCATNGCATCCTTCCCCATGGGCTTTACCGA 450

AAGCGCCACGAAAANGGCCTCGGAAAAGNCAATTTTTACNGGCTCCACTT 500

TGCNTTTTTCAANTATGCNGANCTGNACCGGACGGTNANAATGTACANGA 550

ACCTTGTACGTCNNCAAGACATTTAGGTTGTGACCGNTTAGCATNAGCNG 600

TNNTAAACAGTAGAACAATGTGTGANCCNTAACTAAAAAATANACAGCGT 650

TAAAATCACGATTCTGGATGAAAATGATCATGCAATANCCGAAAGCGAAG 700

GCGCTAAAGGCAATGTAACTATTCAAAATCCTATATTGTGGCAACCTTTA 750

CATGCCTATTTATACAATATGAAAGTAGAATTACTCAACGATAATGAGTG 800

TGTAGATGTTTATACAGAACGTTTCGGTATTCGATCTGTNGAAGTGAAGG 850

ATGGACAGTTTTTAATTAATGACAAACCATTTTATTTCAAAGGTTTCGGT 900

AAACATGAAGATACCTATTAAAATGGTCGAGGCTTAAACGAATCAGCCAA 950

CGTCATGGACATCAACTTAATGAAATGGATAGGTGCTAATTCATTTAGAA 1000

CCTCTCATTACCCATATTCAGAAGAAATGATGCGTTTAGCAGATGAACAA 1050

GGTATTGTAGTGATAGATGAGACAACANGTGTCGGTATACATCTTAATTT 1100

TATGGNNACCTTAGGTGGCTCCNTTGCACATGATACATGGAANGAATTTG 1150

ACACTCTCGAGTTTCATAAAGAAGTCATANAAGACTTGATTGNGAGAGAC 1200

AAGAATCATGCATGGGTAGTCATGTGGTNATTTGGCAATGAGCNAGGGTN 1250

AAATAAAGGGGGTGCTAAAGCATNCTTTGAGCCATTTGTTAATTTAGCAG 1300

GTGAAAAAGATNNTCNGNNTNGCCCAGTGACTATCGTTACTATATTANCT 1350

GCNNANCGAAATGTATGTGAAGTTNNAGATTTAGTCGATGTGGTTTGTCT 1400

FIGURE 4H

```
NNNNAGNNNNTANGGTTGGTATNCACAATCAGGTGATTTAGAAGGTGCTA 1450

AACNAGCATTAGATAAGGAGNTAGNCGAATGGTGGAAANGACAACNAAAT 1500

AAGCCAATNATGTTTACAGAGTATGGTGTGGATANNGTTGTAGGTTTACA 1550

NNCGATNCCTGATAAAATGCNNCCAGAAGAGTATAAAATGAGNTTTTATA 1600

AAGGNTATNATAAAATTATGGATAAACGATCGCAGCTGAGTACACGAGCT 1650

CACCCGCGGAGTCGACAAGATCCAAGTACTACCCGGGNATACGTAACTAG 1700

TGCATGCTCGCGAAATATTTAGGCCTTATCGAATTAAT              1739
```

***Staphylococcus homini* ß-glucuronidase gene**

```
TGTGGGNCTTTGTTCCTTGNTCAGCTCCCCAACGGCTTGAAGTACTCGTA  50

CGCGCCCTCTTCCTCAGTCGCCGCCTCGTTGGCGATGCTCCACATCACGA 100

CGCTTGGATGGTTCTTGTCACGAGACACCAGTTCACGGAGAACGTCTTGA 150

TGGTGCTCAAACGTCCGAATCTTCTCCCAGGTACTGACGCGCTCGCTGCC 200

TTCGCCGAGTCCCGTGGTGGCCATGAAGTTGAGGTGCACGCCAACTGCCG 250

GAGTCTCGTCGATCACGACCAGACCCTCGCGATCCGCAAGACGCATCAAC 300

TCTTCAGAGTACGGATAGTGTGCGGTCCGGAAGCTGTTGGCGCCGATCCA 350

TTTGAGGATATTGAAATCCATCACATTGCTCGCTTCGTTAAAGCCACGGC 400

CGTTGATAGGAGTGTCCTCATGTTTGCCAAAGCCCTTGAAGTAGAACGGT 450

TTGTTGTTGATGAGGAACTTGCCGTCGTTGACTTCACGGTCCGCACGCCG 500

AACGGCTCTTCATAGACATCGATGGTCAAGTCCCGTCGTTCACCAGTTCC 550

ACTTTGATCTGGTAGAGATACGTGTTCAAGTGGTTCCCAGAGGATGACAT 600

TCGGAATCTTCACGTTACCGCTCAAGCC                        629
```

FIGURE 4I

Thermotoga maritima ß-glucuronidase

ATGGTAAGACCGCAACGAAACAAGAAGAGATTTATTCTTATCTTGAATGG 50

AGTTTGGAATCTTGAAGTAACCAGCAAAGACAGACCAATCGCCGTTCCTG 100

GAAGCTGGAATGAGCAGTACCAGGATCTGTGCTACGAAGAAGGACCCTTC 150

ACCTACAAAACCACCTTCTACGTTCCGAAGNAACTTTCACAAAAACACAT 200

CAGACTTTACTTTGCTGCGGTGAACACGGACTGCGAGGTCTTCCTCAACG 250

GAGAGAAAGTGGGAGAGAATCACATTGAATACCTTCCCTTCGAAGTAGAT 300

GTGACGGGGAAAGTGAAATCCGGAGAGAACGAACTCAGGGTGGTTGTTGA 350

GAACAGATTGAAAGTGGGAGGATTTCCCTCGAAGGTTCCAGACAGCGGCA 400

CTCACACCGTGGGATTTTTTGGAAGTTTTCCACCTGCAAACTTCGACTTC 450

TTCCCCTACGGTGGAATCATAAGGCCTGTTCTGATAGAGTTCACAGACCA 500

CGCGAGGATACTCGACATCTGGGTGGACACGAGTGAGTCTGAACCGGAGA 550

AGAAACTTGGAAAAGTGAAAGTGAAGATAGAAGTCTCAGAAGAAGCGGTG 600

GGACAGGAGATGACGATCAAACTTGGAGAGGAAGAGAAAAAGATTAGAAC 650

ATCCAACAGATTCGTCGAAGGGGAGTTCATCCTCGAAAACGCCAGGTTCT 700

GGAGCCTCGAAGATCCATATCTTTATCCTCTCAAGGTGGAACTTGAAAAA 750

GACGAGTACACTCTGGACATCGGAATCAGAACGATCAGCTGGGACGAGAA 800

GAGGCTCTATCTGAACGGGAAACCTGTCTTTTTGAAGGGCTTTGGAAAGC 850

ACGAGGAATTCCCCGTTCTGGGGCAGGGCACCTTTTATCCATTGATGATA 900

AAAGACTTCAACCTTCTGAAGTGGATCAACGCGAATTCTTTCAGGACCTC 950

TCACTATCCTTACAGTGAAGAGTGGCTGGATCTTGCCGACAGACTCGGAA 1000

TCCTTGTGATAGACGAAGCCCCGCACGTTGGTATCACAAGGTACCACTAC 1050

AATCCCGAGACTCAGAAGATAGCAGAAGACAACATAAGAAGAATGATCGA 1100

CAGACACAAGAACCATCCCAGTGTGATCATGTGGAGTGTGGCGAACGAAC 1150

CAGAGTCCAACCATCCAGACGCGGAGGGTTTCTTCAAAGCCCTTTATGAG 1200

FIGURE 4J


```
ACTGCCAATGAAATGGATCGAACACGCCCCGTTGTCATGGTGAGCATGAT 1250

GGACGCACCAGACGAGAGAACAAGAGACGTGGCGCTGAAGTACTTCGACA 1300

TCGTCTGTGTGAACAGGTACTACGGCTGGTACATCTATCAGGGAAGGATA 1350

GAAGAAGGACTTCAAGCTCTGGAAAAAGACATAGAAGAGCTCTATGCAAG 1400

GCACAGAAAGCCCATCTTTGTCACAGAATTCGGTGCGGACGCGATAGCTG 1450

GCATCCACTACGATCCACCTCAAATGTTCTCCGAAGAGTACCAAGCAGAG 1500

CTCGTTGAAAAGACGATCAGGCTCCTTTTGAAAAAAGACTACATCATCGG 1550

AACACACGTGTGGGCCTTTGCAGATTTTAAGACTCCTCAGAATGTGAGAA 1600

GACCCATTCTCAACCACAAGGGTGTTTTCACAAGAGACAGACAACCCAAA 1650

CTCGTTGCTCATGTACTGAGAAGACTGTGGAGTGAGGTT             1689
```

```
BGUS        ------MLYPINTETRGVFDLNGVWNFKLDYG----KGLEEKWYESKLTDT---ISMAVP 47
HGUS        LGLQGGMLYPQESPSRECKELDGLWSFRADFSDNRRRGFEEQWYRRPLWESGPTVDMPVP 60
EGUS        ------MLRPVETPTREIKKLDGLWAFSLDREN---CGIDQRWWESALQESR---AIAVP 48

BGUS        SSYNDIGVTKEIRNHIGYVWYEREFTVPAYLKD---QRIVLRFGSATHKAIVYVNGELVV 104
HGUS        SSFNDISQDWRLRHFVGWVWYEREVILPERWTQDLRTRVVLRIGSAHSYAIVWVNGVDTL 120
EGUS        GSFNDQFADADIRNYAGNVWYQREVFIPKGWAG---QRIVLRFDAVTHYGKVWVNNQEVM 105

BGUS        EHKGGFLPFEAEINNSLRDG----MNRVTVAVDNILDDSTLPVG-LYSERHEEGLGKVIR 159
HGUS        EHEGGYLPFEADISNLVQVGPLPSRLRITIAINNTLTPTTLPPGTIQYLTDTSKYPKGYF 180
EGUS        EHQGGYTPFEADVTPYVIAG---KSVRITVCVNNELNWQTIPPG--MVITDENGKKK--- 157

BGUS        -NKPNFDFFNYAGLHRPVKIYTTPFTYVEDISVVTDFNGPT--GTVTYTVDFQG-KAETV 215
HGUS        VQNTYFDFFNYAGLQRSVLLYTTPTTYIDDITVTTSVEQDS--GLVNYQISVKGSNLFKL 238
EGUS        -QSYFHDFFNYAGIHRSVMLYTTPNTWVDDITVVTHVAQDCNHASVDWQVVANG----DV 212

BGUS        KVSVVDEEGKVVASTEGLSGNVEIPNVILWEP-----LNTYLYQIKVELVNDGLT---ID 267
HGUS        EVRLLDAENKVVANGTGTQGQLKVPGVSLWWPYLMHERPAYLYSLEVQLTAQTSLGPVSD 298
EGUS        SVELRDADQQVVATGQGTSGTLQVVNPHLWQP-----GEGYLYELCVTAKSQTEC----D 263

BGUS        VYEEPFGVRTVEVNDGKFLINNKPFYFKGFGKHEDTPINGRGFNEASNVMDFNILKWIGA 327
HGUS        FYTLPVGIRTVAVTKSQFLINGKPFYFHGVNKHEDADIRGKGFDWPLLVKDFNLLRWLGA 358
EGUS        IYPLRVGIRSVAVKGEQFLINHKPFYFTGFGRHEDADLRGKGFDNVLMVHDHALMDWIGA 323

BGUS        NSFRTAHYPYSEELMRLADREGLVVIDETPAVGVHLNFMATTGLGEGSERVSTWEKIR-- 385
HGUS        NAFRTSHYPYAEEVMQMCDRYGIVVIDECPGVGLAL----------P------QFFNNV 401
EGUS        NSYRTSHYPYAEEMLDWADEHGIVVIDETAAVGFNLSLGIGFEAGNKPKELYSEEAVNGE 383

BGUS        TFEHHQDVLRELVSRDKNHPSVVMWSIANEAATEEEGAYEYFKPLVELTKELDPQKRPVT 445
HGUS        SLHHHMQVMEEVVRRDKNHPAVVMWSVANEPASHLESAGYYLKMVIAHTKSLDPS-RPVT 460
EGUS        TQQAHLQAIKELIARDKNHPSVVMWSIANEPDTRPQGAREYFAPLAEATRKLDPT-RPIT 442

BGUS        IVLFVMATPETDKVAELIDVIALNRYNGWYFDGGDLEAAKVHLRQEFHAWNKRCPGKPIM 505
HGUS        FVS--NSNYAADKGAPYVDVICLNSYYSWYHDYGHLELIQLQLATQFENWYKKYQ-KPII 517
EGUS        CVNVMFCDAHTDTISDLFDVLCLNRYYGWYVQSGDLETAEKVLEKELLAWQEKLH-QPII 501

BGUS        ITEYGADTVAGFHDIDPVMFTEEYQVEYYQANHVVFD--EFENFVGEQAWNFADFATSQG 563
HGUS        QSEYGAETIAGFHQDPPLMFTEEYQKSLLEQYHLGLDQKRRKYVVGELIWNFADFMTEQS 577
EGUS        ITEYGVDTLAGLHSMYTDMWSEEYQCAWLDMYHRVFD--RVSAVVGEQVWNFADFATSQG 559

BGUS        VMRVQGNKKGVFTRDRKPKLAAHVFRERWTNIPDFGYKN----- 602
HGUS        PTRVLGNKKGIFTRQRQPKSAAFLLRERYWKIAN-ET------- 613
EGUS        ILRVGGNKKGIFTRDRKPKSAAFLLQKRWTGMNFGEKPQQGGKQ 603
```

FIGURE 5

09/936759

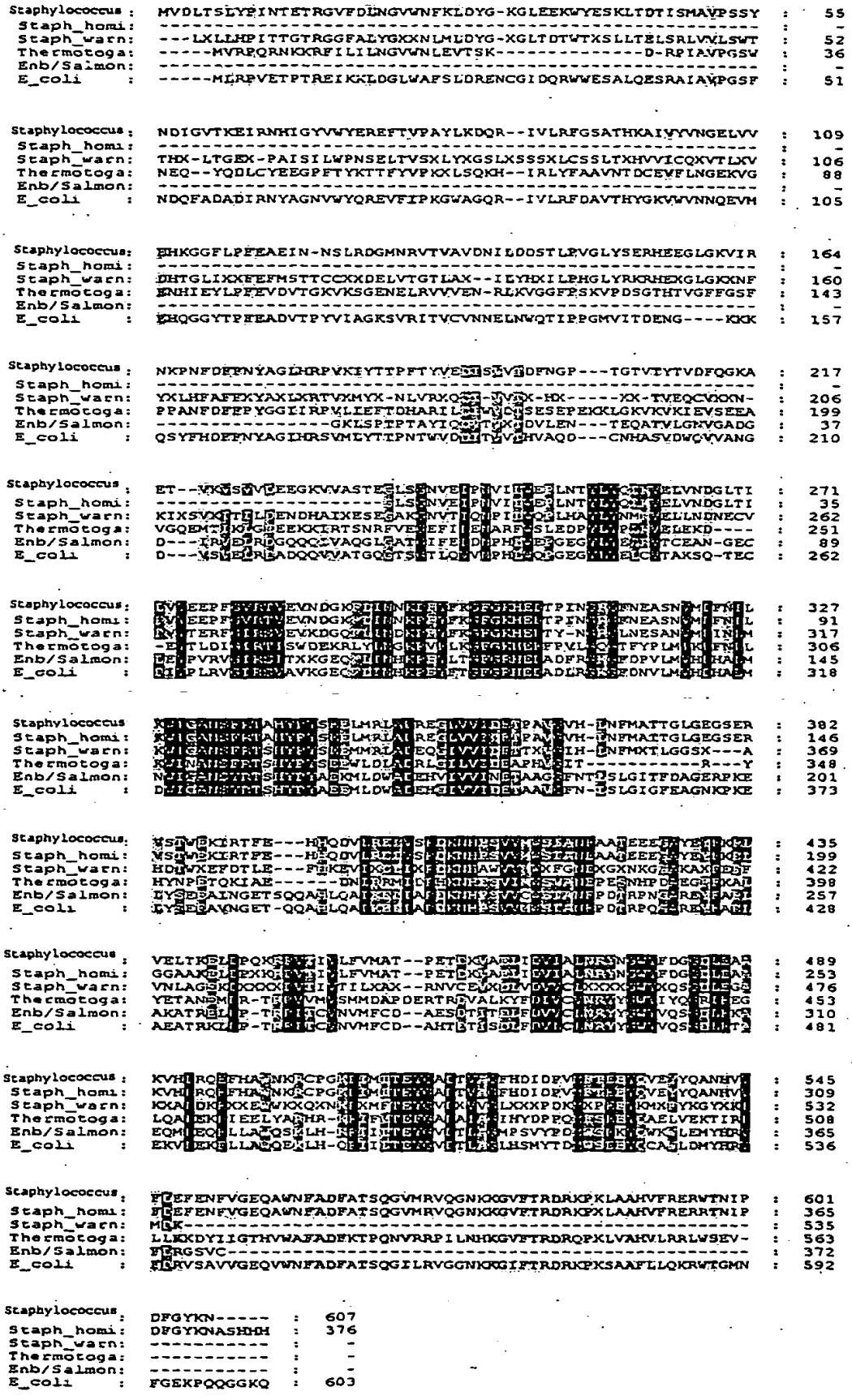

FIGURE 5C

09936759 Title: MICROBIAL B-GLUCURONIDASE GENES, GENE PRODUCTS AND USES THEREOF
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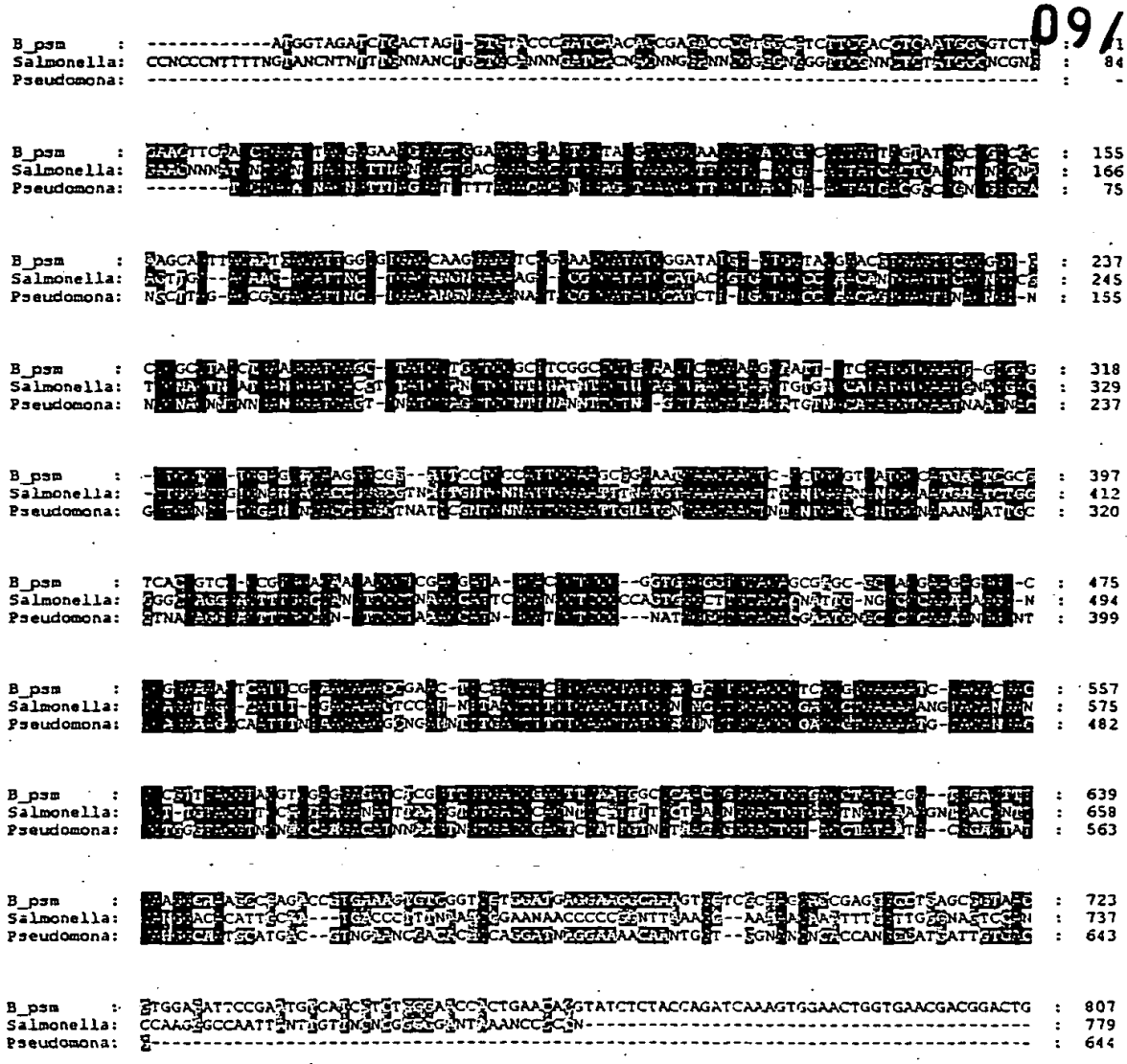
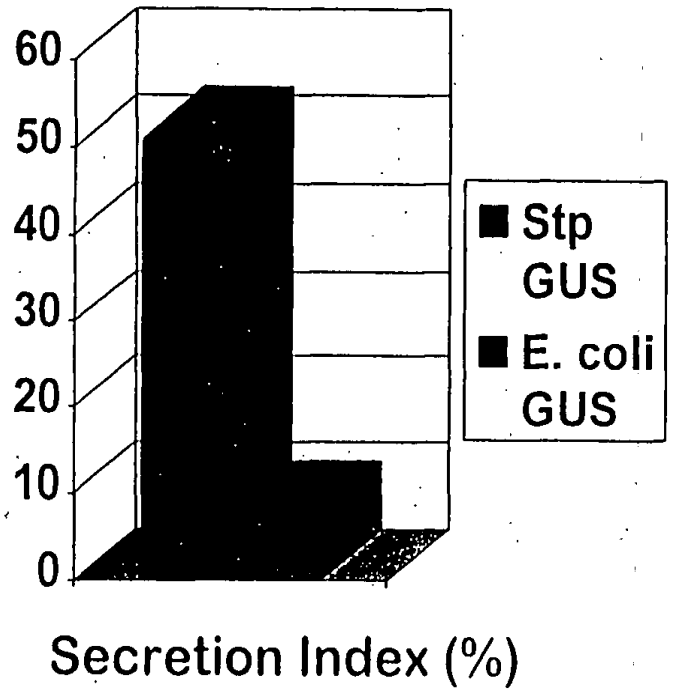


Secretion of GUS^{Stp} in *E. coli*



Cellular fractions were assayed for glucuronidase and galactosidase activity

Secretion Index was calculated as follows:

- percent of total activity in the periplasm fraction for glucuronidase and galactosidase was calculated
- galactosidase value was subtracted from glucuronidase as "contamination"

FIG. 6

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Title: MICROBIAL BETA-GLUCURONIDASE GENES, GENE PRODUCTS AND USES THEREOF
Inventor(s): JEFFERSON ET AL.
DOCKET NO.: 076518-0150

Title: MICROBIAL B-GLUCURONIDASE GENES, GENE PRODUCTS AND USES THEREOF
Inventor(s): JEFFERSON ET AL.
DOCKET NO.: 076518-0150

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FIG. 7

Title: MICROBIAL B-GLUCURONIDASE GENES, GENE PRODUCTS AND USES THEREOF
Inventor(s): JEFFERSON ET AL.
DOCKET NO.: 076518-0150

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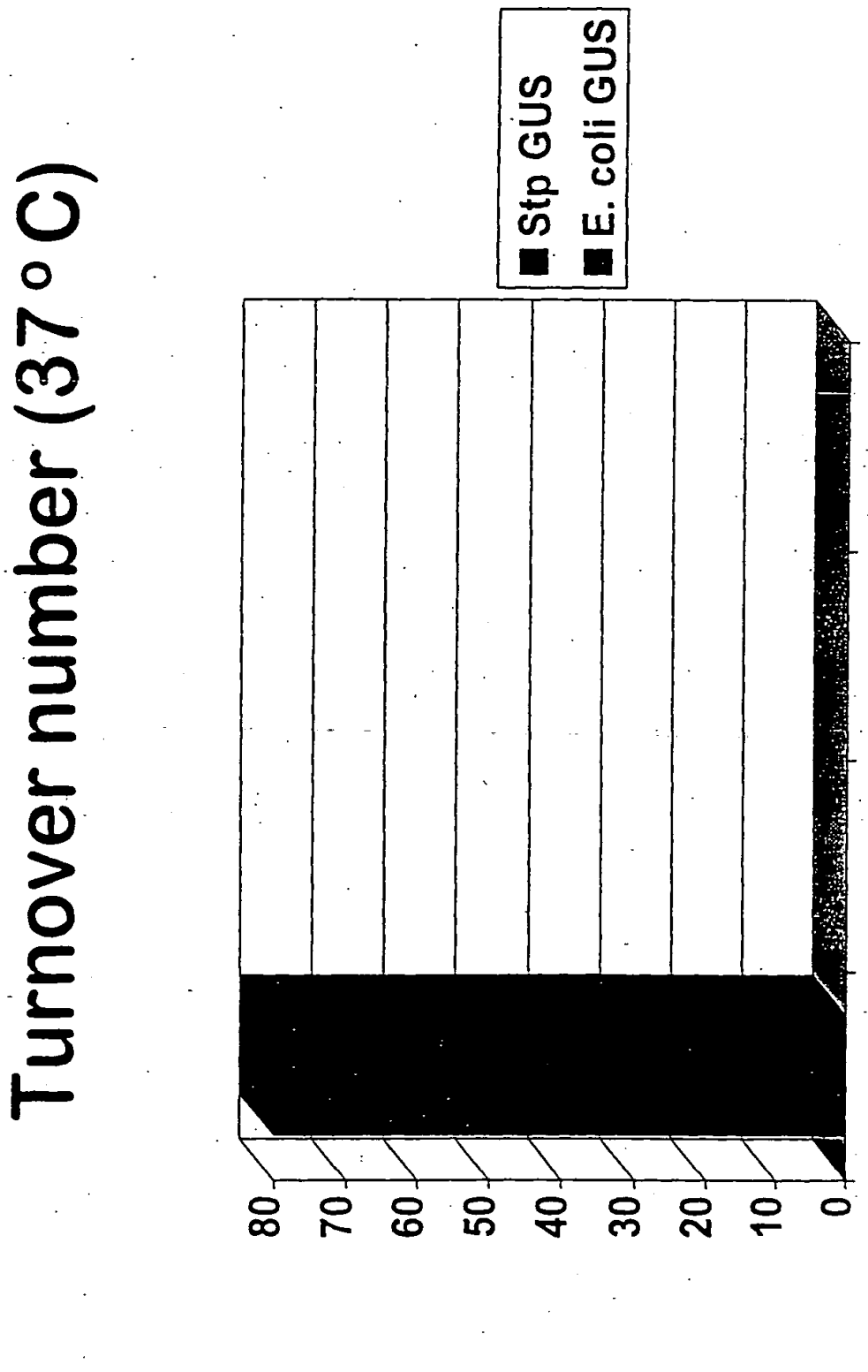

FIG. 8

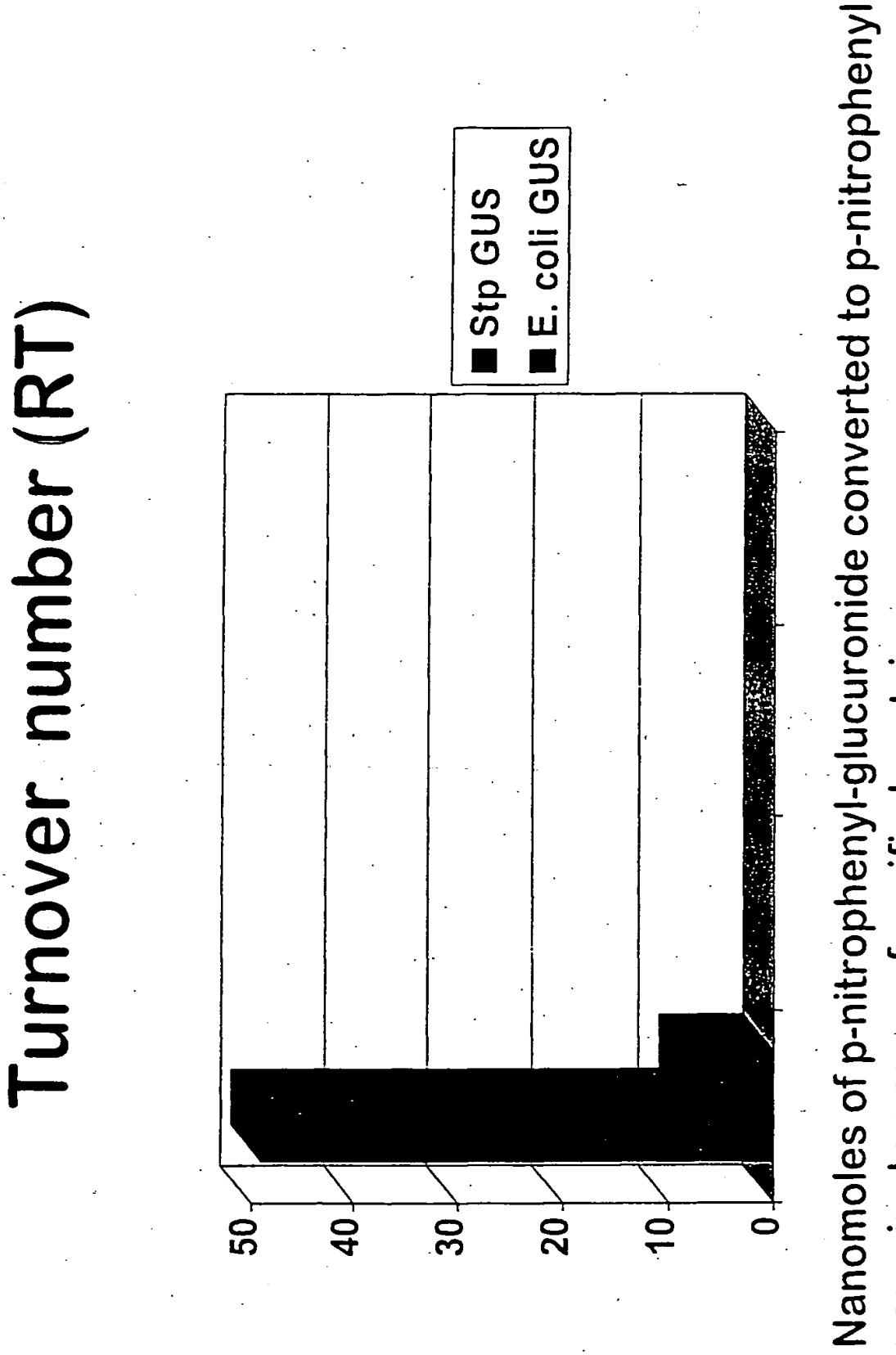
Turnover number (RT)
Stp GUS
E. coli GUS
50
40
30
20
10
0
Nanomoles of p-nitrophenyl-glucuronide converted to p-nitrophenyl per minute per µg of purified protein

FIG. 9

09936759 Title: MICROBIAL B-GLUCURONIDASE GENES, GENE PRODUCTS AND USES THEREOF
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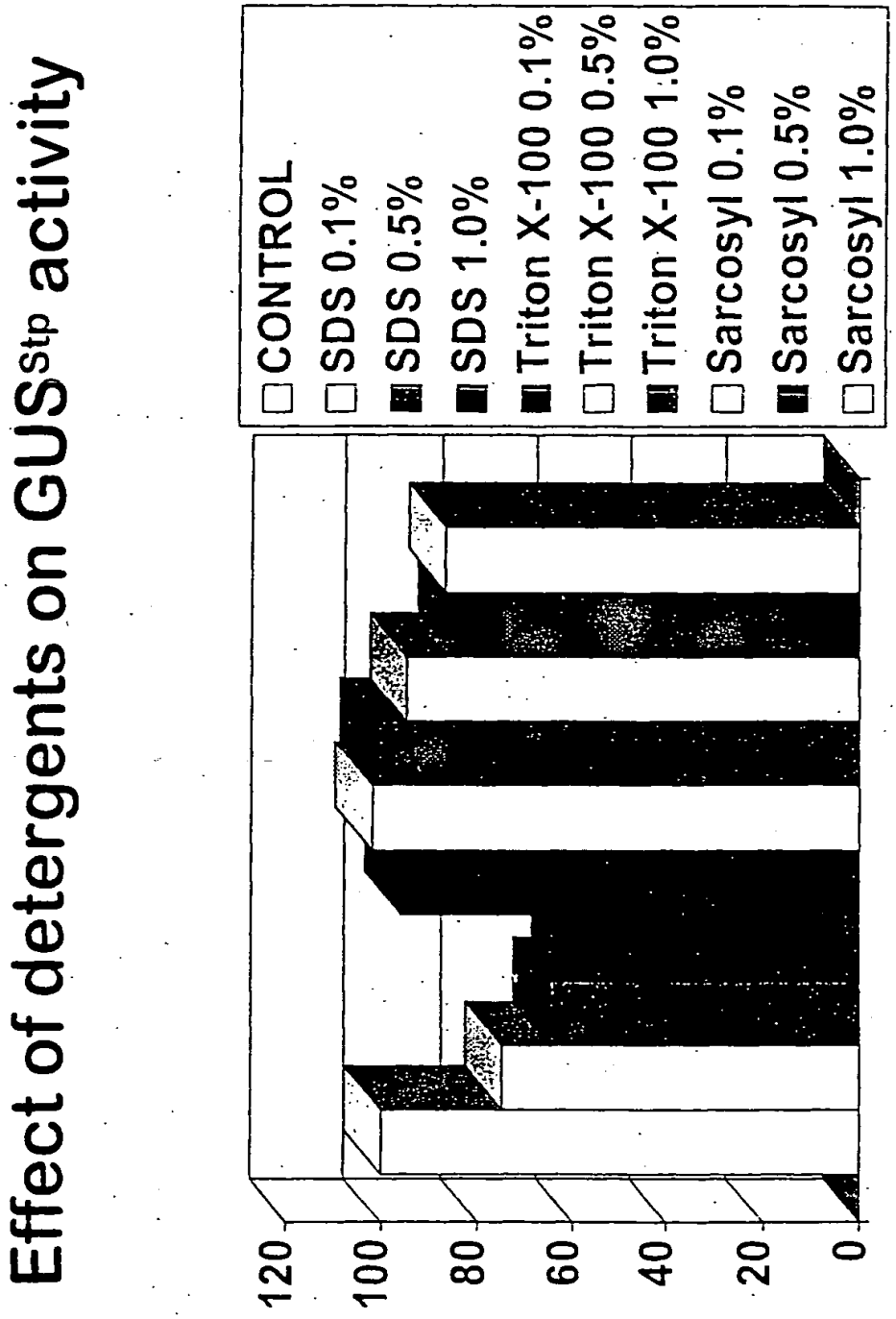

FIG. 10

09936759 Title: MICROBIAL B-1 GLUCURONIDASE GENES, GENE PRODUCTS AND USES THEREOF
Inventor(s): JEFFERSON ET AL.
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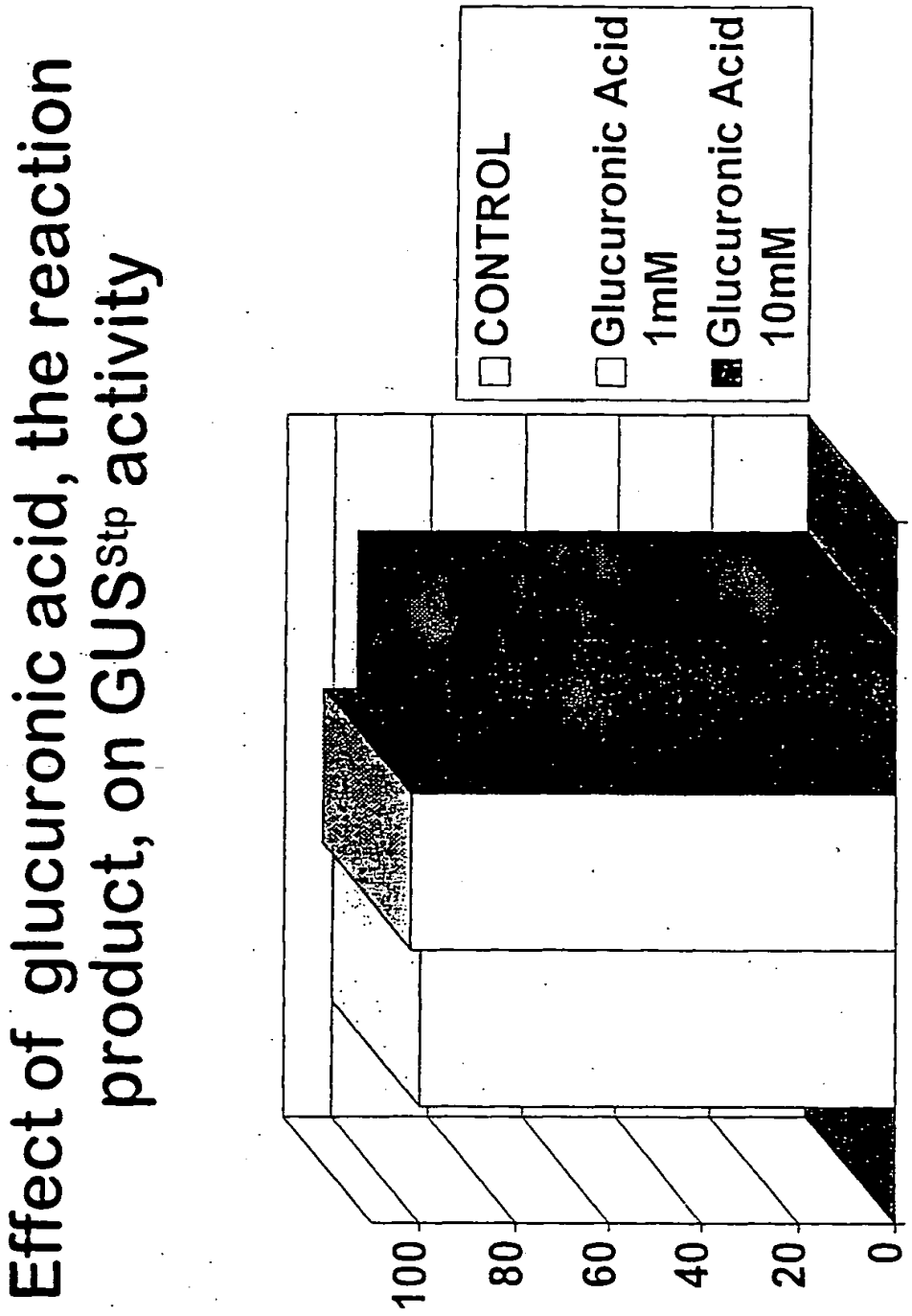

FIG. 11

09936759 Title: MICROBIAL B-GLUCURONIDASE GENES, GENE PRODUCTS AND USES THEREOF
Inventor(s): JEFFERSON ET AL.
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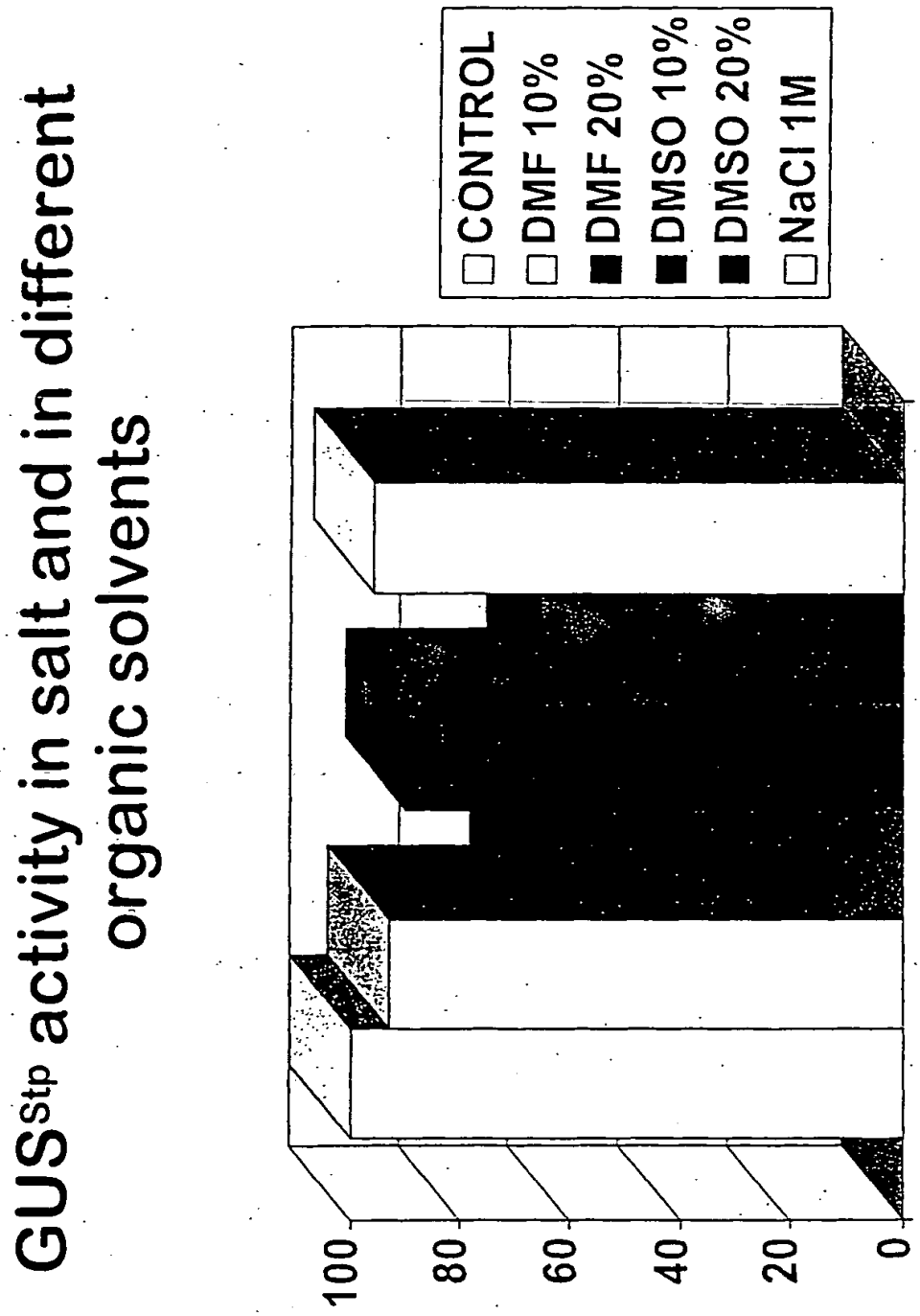

FIG. 12

FIGURE 13A

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```
                                                    MetValAspLeuThrSerLeuTyr
ATACGACTCA CTAGTGGGTC GACCCATGGTAGATCTGACTAGTCTGTAC
                    SalI    NcoI    BglII

ProIleAsnThrGluThrArgGlyValPheAspLeuAsnGlyValTrpAsn
CCGATCAACACCGAGACCCGTGGCGTCTTCGACCTCAATGGCGTCTGGAAC

PheLysLeuAspTyrGlyLysGlyLeuGluGluLysTrpTyrGluSerLys
TTCAAGCTGGACTACGGGAAAGGACTGGAAGAGAAGTGGTACGAAAGCAA

LeuThrAspThrIleSerMetAlaValProSerSerTyrAsnAspIle
GCTGACCGACACTATTAGTATGGCCGTCCCAAGCAGTTACAATGACATTG

GlyValThrLysGluIleArgAsnHisIleGlyTyrValTrpTyrGluArg
GCGTGACCAAGGAAATCCGCAACCATATCGGATATGTCTGGTACGAACGT

GluPheThrValProAlaTyrLeuLysAspGlnArgIleValLeuArgPhe
GAGTTCACGG TGCCGGCCTATCTGAAGGATCAGCGTATCGTGCTCCGCTT

GlySerAlaThrHisLysAlaIleValTyrValAsnGlyGluLeuVal
CGGCTCTGCAACTCACAAAGCAATTGTCTATGTCAATGGTGAGCTGGTCG

ValGluHisLysGlyGlyPheLeuProPheGluAlaGluIleAsnAsnSer
TGGAGCACAAGGGCGGATTCCTGCCATTCGAAGCGGAAATCAACAACTCG

LeuArgAspGlyMetAsnArgValThrValAlaValAspAsnIleLeuAsp
CTGCGTGATGGCATGAATCGCGTCACCGTCGCCGTGGACAACATCCTCGA

AspSerThrLeuProValGlyLeuTyrSerGluArgHisGluGluGly
CGATAGCACCCTCCCGGTGGGGCTGTACAGCGAGCGCCACGAAGAGGGCC

LeuGlyLysValIleArgAsnLysProAsnPheAspPhePheAsnTyrAla
TCGGAAAAGTCATTCGTAACAAGCCGAACTTCGACTTCTTCAACTATGCA

GlyLeuHisArgProValLysIleTyrThrThrProPheThrTyrValGlu
GGCCTGCACCGTCCGGTGAAAATCTACACGACCCCGTTTACGTACGTCGA

AspIleSerValValThrAspPheAsnGlyProThrGlyThrValThr
GGACATCTCGGTTGTGACCGACTTCAATGGCCCAACCGGGACTGTGACCT

TyrThrValAspPheGlnGlyLysAlaGluThrValLysValSerValVal
ATACGGTGGACTTTCAAGGCAAAGCCGAGACCGTGAAAGTGTCGGTCGTG

AspGluGluGlyLysValValAlaSerThrGluGlyLeuSerGlyAsnVal
GATGAGGAAGGCAAAGTGGTCGCAAGCACCGAGGGCCTGAGCGGTAACGT

GluIleProAsnValIleLeuTrpGluProLeuAsnThrTyrLeuTyr
GGAGATTCCGAATGTCATCCTCTGGGAACCACTGAACACGTATCTCTACC
```

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FIGURE 13B

GlnIleLysValGluLeuValAsnAspGlyLeuThrIleAspValTyrGlu
CAGATCAAAGTGGAACTGGTGAACGACGGACTGACCATCGATGTCTATGAA

GluProPheGlyValArgThrValGluValAsnAspGlyLysPheLeuIle
GAGCCGTTCGGCGTGCGGACCGTGGAAGTCAACGACGGCAAGTTCCTCAT

AsnAsnLysProPheTyrPheLysGlyPheGlyLysHisGluAspThr
CAACAACAAACCGTTCTACTTCAAGGGCTTTGGCAAACATGAGGACACTC

ProIleAsnGlyArgGlyPheAsnGluAlaSerAsnValMetAspPheAsn
CTATCAACGGCCGTGGCTTTAACGAAGCGAGCAATGTGATGGATTTCAAT

IleLeuLysTrpIleGlyAlaAsnSerPheArgThrAlaHisTyrProTyr
ATCCTCAAATGGATCGGCGCCAACAGCTTCCGGACCGCACACTATCCGTA

SerGluGluLeuMetArgLeuAlaAspArgGluGlyLeuValValIle
CTCTGAAGAGTTGATGCGTCTTGCGGATCGCGAGGGTCTGGTCGTGATCG

AspGluThrProAlaValGlyValHisLeuAsnPheMetAlaThrThrGly
ACGAGACTCCGGCAGTTGGCGTGCACCTCAACTTCATGGCCACCACGGGA

LeuGlyGluGlySerGluArgValSerThrTrpGluLysIleArgThrPhe
CTCGGCGAAGGCAGCGAGCGCGTCAGTACCTGGGAGAAGATTCGGACGTT

GluHisHisGlnAspValLeuArgGluLeuValSerArgAspLysAsn
TGAGCACCATCAAGACGTTCTCCGTGAACTGGTGTCTCGTGACAAGAACC

HisProSerValValMetTrpSerIleAlaAsnGluAlaAlaThrGluGlu
ATCCAAGCGTCGTGATGTGGAGCATCGCCAACGAGGCGGCGACTGAGGAA

GluGlyAlaTyrGluTyrPheLysProLeuValGluLeuThrLysGluLeu
GAGGGCGCGTACGAGTACTTCAAGCCGTTGGTGGAGCTGACCAAGGAACT

AspProGlnLysArgProValThrIleValLeuPheValMetAlaThr
CGACCCACAGAAGCGTCCGGTCACGATCGTGCTGTTTGTGATGGCTACCC

ProGluThrAspLysValAlaGluLeuIleAspValIleAlaLeuAsnArg
CGGAGACGGACAAAGTCGCCGAACTGATTGACGTCATCGCGCTCAATCGC

TyrAsnGlyTrpTyrPheAspGlyGlyAspLeuGluAlaAlaLysValHis
TATAACGGATGGTACTTCGATGGCGGTGATCTCGAAGCGGCCAAAGTCCA

LeuArgGlnGluPheHisAlaTrpAsnLysArgCysProGlyLysPro
TCTCCGCCAGGAATTTCACGCGTGGAACAAGCGTTGCCCAGGAAAGCCGA

IleMetIleThrGluTyrGlyAlaAspThrValAlaGlyPheHisAspIle
TCATGATCACTGAGTACGGCGCAGACACCGTTGCGGGCTTTCACGACATT

AspProValMetPheThrGluGluTyrGlnValGluTyrTyrGlnAlaAsn
GATCCAGTGATGTTCACCGAGGAATATCAAGTCGAGTACTACCAGGCGAA

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Inventor(s): JEFFERSON ET AL.
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FIGURE 13C

```
  HisValValPheAspGluPheGluAsnPheValGlyGluGlnAlaTrp
 CCACGTCGTGTTCGATGAGTTTGAGAACTTCGTGGGTGAGCAAGCGTGGA

AsnPheAlaAspPheAlaThrSerGlnGlyValMetArgValGlnGlyAsn
 ACTTCGCGGACTTCGCGACCTCTCAGGGCGTGATGCGCGTCCAAGGAAAC

 LysLysGlyValPheThrArgAspArgLysProLysLeuAlaAlaHisVal
 AAGAAGGGCGTGTTCACTCGTGACCGCAAGCCGAAGCTCGCCGCGCACGT

  PheArgGluArgTrpThrAsnIleProAspPheGlyTyrLysAsn
 CTTTCGCGAGCGCTGGACCAACATTCCAGATTTCGGCTACAAGAACGCTA

SerHisHisHisHisHisHisVal *
 GCCATCACCATCACCATCACGTGTGAATTGGTGACCG
 NheI               PmlI      BstEII
```

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DOCKET NO.: 076518-0150

09/936759

FIGURE 14

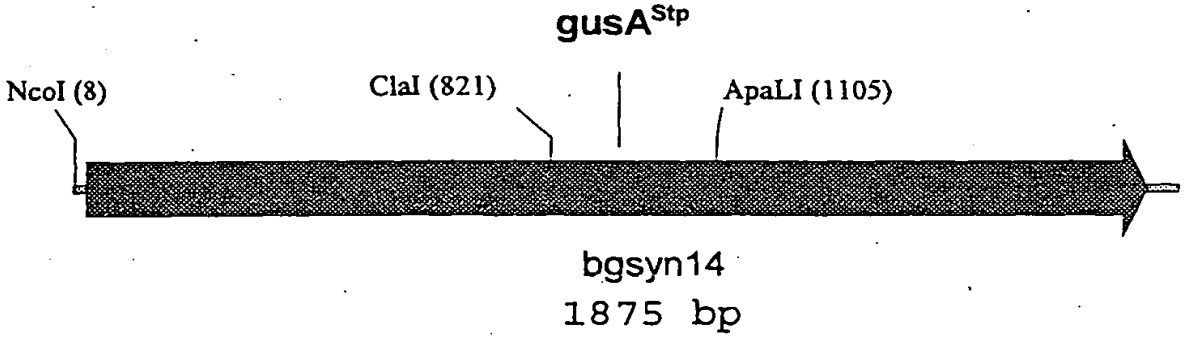
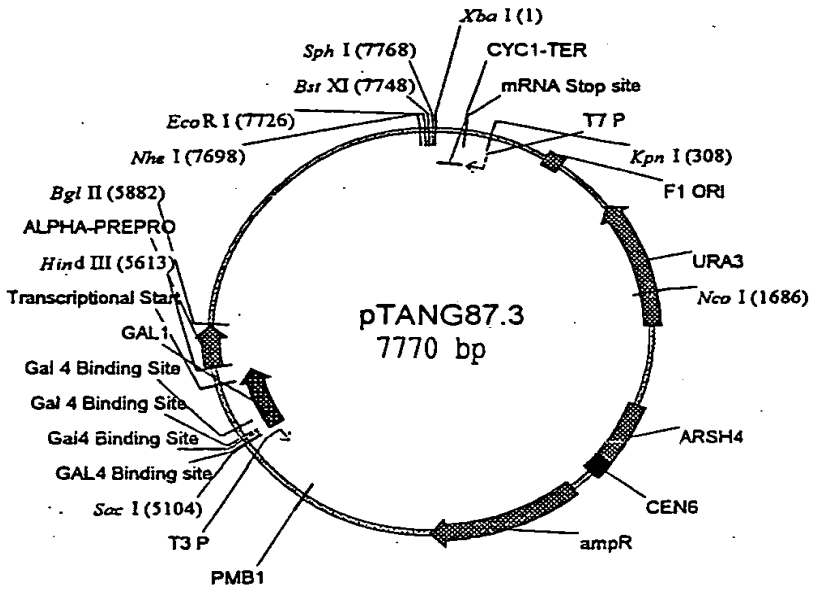


FIGURE 15


Xba I (1)
Sph I (7768)
CYC1-TER
Bst XI (7748)
mRNA Stop site
EcoR I (7726)
T7 P
Nhe I (7698)
Kpn I (308)
F1 ORI
Bgl II (5882)
ALPHA-PREPRO
URA3
Hind III (5613)
Nco I (1686)
Transcriptional Start
pTANG87.3
7770 bp
GAL1
Gal 4 Binding Site
Gal 4 Binding Site
ARSH4
Gal4 Binding Site
GAL4 Binding site
CEN6
Sac I (5104)
T3 P
ampR
PMB1

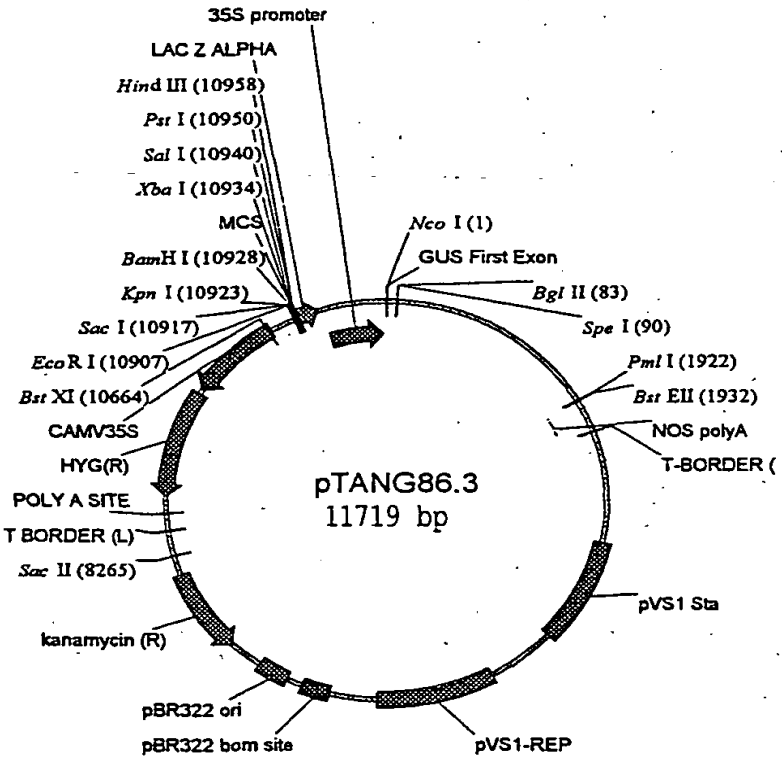

3SS promoter
LAC Z ALPHA
Hind III (10958)
Pst I (10950)
Sal I (10940)
Xba I (10934)
MCS
Nco I (1)
BamH I (10928)
GUS First Exon
Kpn I (10923)
Bgl II (83)
Sac I (10917)
Spe I (90)
EcoR I (10907)
Pml I (1922)
Bst XI (10664)
Bst EII (1932)
CAMV35S
NOS polyA
HYG(R)
T-BORDER (
pTANG86.3
11719 bp
POLY A SITE
T BORDER (L)
Sac II (8265)
pVS1 Sta
kanamycin (R)
pBR322 ori
pBR322 bom site
pVS1-REP

FIGURE 16

```
   1  ATGTTACGTT CTGTCGAAAC CGCGACGCGA GAAATCAAAA AACTGGACGG
  51  CCTGTGGTCG TTTTGTATGG ATAGCGAAGA GTGCGGCAAC GCGCAGCAAT
 101  GGTGGCGTCA ACCGTTACCC CAAAGCCGCG CTATCGCCGT TCCGGGAAGC
 151  TATAACGATC AGTTTGCCGC TGCCGAGATC CGCAATTATG TTGGCAACGT
 201  CTGGTATCAG CGTGAGATAC GCATCCCGAA AGGCTGGGAT CGCCAGCGCA
 251  TAGTGCTGCG CTTTGATGCG GTGACTCACT ATGGAAAAGT TTGGGTCAAT
 301  GACCAATTTT TAATGGAACA TCAGGGCGGC TACACGCCGT TTGAAGCGGA
 351  TATCAGCCAC CTTATCTCCG CCGGGGAATC CGTGCGTATC ACGGTATGCG
 401  TGAATAACGA GCTGAACTGG CAGACGATCC CGCCGGGCGT TGTGACCCAG
 451  GGCGTAAACG GTAAGAAGCA GCAAGCGTAT TTCCATGATT TCTTTAACTA
 501  CGCCGGTATT CATCGCAGCG TAATGCTGTA CACCACGCCG AAAACTTTTG
 551  TGGAAGATAT TACCGTCGTG ACGCAGGTTG CTGACGATCT GGCTCAGGCT
 601  ACCGTCGCCT GGCAGGTACG GGCGAATGGC GAAGTGCGTG TAGAGCTACG
 651  TGACGCGGAG CAACAGCTTG TCGCTTCGGG GCAAGGGGAA AAAGGTGAAC
 701  TGCTGCTGGA AGGGCCGCGG CTGTGGCAGC CTGGCGAGGG CTATCTTTAT
 751  GAACTGCGGG TCATCGCGCA GCATCAGGAC GAGCAGGATG AATATCCGCT
 801  GCGCGTCGGT ATTCGCTCGG TAGAAGTAAA AGGGGAGCAG TTCCTGATCA
 851  ACCATAAGCC TTTCTATTTC ACCGGGTTCG GACGTCATGA AGATGCCGAT
 901  CTGCGCGGTA AGGGTTTTGA TAACGTGCTG ATGGTGCACG ACCACGCGCT
 951  AATGGACTGG ATCGGTGCGA ACTCTTACCG TACCTCGCAT TACCCTTATG
1001  CCGAAGAGAT GCTCGACTGG GCGGACGAAC ATGGCATCGT CATCATTGAT
1051  GAAACGGCCG CCGTCGGATT CAACCTGTCT TTAGGGATTA GCTTTGATGT
1101  CGGCGAAAAA CCCAAAGAGC TCTACAGCGA TGAGGCCGTG AACGATGAAA
1151  CGCAGCGCGC GCACCTGCAG GCAATTAAGG AGCTGATTGC CCGCGATAAG
1201  AACCACCCAA GCGTCGTGAT GTGGAGTATC GCCAACGAAC CGGATACCCG
1251  CCCGAACGGC GCGCGCGAAT ACTTCGCTCC GCTGGCGCAG GCAACGCGCG
1301  AACTCGATCC TACACGTCCG ATAACCTGCG TGAACGTGAT GTTCTGCGAT
1351  GCGGAAAGCG ACACCATTAC CGATCTCTTT GATGTCGTTT GCCTGAACCG
1401  CTACTACGGC TGGTATGTAC AAAGCGGCGA TCTGGAGAAG GCTGAGAAAG
1451  TGCTGGAGAA AGAGCTTCTG GCCTGGCAGG AGAAACTCCA CCGCCCGATT
1501  ATCATCACCG AATACGGCGT CGATACGCTT GCAGGCCTGC ATTCCATGTA
1551  CAACGATATG TGGAGCGAAG AGTACCAGTG CGCCTGGCTT GATATGTACC
1601  ATCGCGTGTT TGATCGCGTC AGCGCCGTCG TCGGCGAGCA GGTATGGAAC
1651  TTCGCCGACT TCGCCACTTC GCAGGGCATT ATGCGCGTTG GCGGCAACAA
1701  AAAAGGTATA TTCACCCGCG ACAGAAAACC AAAATCGGCG GCCTTCCTGC
1751  TGCAAAAACG CTGGACCGGC ATGGACTTTG GCGTGAAGCC CCAGCAGGGA
1801  GATAAATAAT GA
```

FIGURE 17

```
  1  MLRSVETATR EIKKLDGLWS FCMDSEECGN AQQWWRQPLP QSRAIAVPGS
 51  YNDQFAAAEI RNYVGNVWYQ REIRIPKGWD RQRIVLRFDA VTHYGKVWVN
101  DQFLMEHQGG YTPFEADISH LISAGESVRI TVCVNNELNW QTIPPGVVTQ
151  GVNGKKQQAY FHDFFNYAGI HRSVMLYTTP KTFVEDITVV TQVADDLAQA
201  TVAWQVRANG EVRVELRDAE QQLVASGQGE KGELLLEGPR LWQPGEGYLY
251  ELRVIAQHQD EQDEYPLRVG IRSVEVKGEQ FLINHKPFYF TGFGRHEDAD
301  LRGKGFDNVL MVHDHALMDW IGANSYRTSH YPYAEEMLDW ADEHGIVIID
351  ETAAVGFNLS LGISFDVGEK PKELYSDEAV NDETQRAHLQ AIKELIARDK
401  NHPSVVMWSI ANEPDTRPNG AREYFAPLAQ ATRELDPTRP ITCVNVMFCD
451  AESDTITDLF DVVCLNRYYG WYVQSGDLEK AEKVLEKELL AWQEKLHRPI
501  IITEYGVDTL AGLHSMYNDM WSEEYQCAWL DMYHRVFDRV SAVVGEQVWN
551  FADFATSQGI MRVGGNKKGI FTRDRKPKSA AFLLQKRWTG MDFGVKPQQG
601  DK
```

09936759 Title: MICROBIAL B-701 GLUCURONIDASE GENES, GENE PRODUCTS AND USES THEREOF
Inventor(s): JEFFERSON ET AL.
DOCKET NO.: 076518-0150

09/936759

```
Staph  :  MVDLTSLYPINTETRGVFDLNGVWNFKLDYG-KGLE  :  35
E coli :  -----MLRPVETPTREIKKLDGLWAFSLDRSNCGID  :  31
Sal    :  -----MLRSVETATREIKKLDGLWSFCMDSEECGNA  :  31

Staph  :  EKWYESKLTDTISMAVPSSYNDIGVTKEIRNHIGYV  :  71
E coli :  QRWWESALQESRATAVPGSFNDQFADADIRNYAGNV  :  67
Sal    :  QQWWRQPLPQSRATAVPGSYNDQFAAAEIRNYVGNV  :  67

Staph  :  WYEREFTVPAYLKDQRIVLRFGSATHKAIVYVNGEL  :  107
E coli :  WYQREVFIPKGWAGQRIVLRFDAVTHYGKVWVNNQE  :  103
Sal    :  WYQREIRIPKGWDRQRIVLRFDAVTHYGKVWVNDQF  :  103

Staph  :  VVEHKGGFLPFEAEINNSLRDGMN-RVTVAVDNILD  :  142
E coli :  VMEHQGGYTPFEADVTPYVIAGKSVRITVCVNNELN  :  139
Sal    :  LMEHQGGYTPFEADISHLISAGESVRITVCVNNELN  :  139

Staph  :  DSTLPVGLYSERHEEGLGKVIRNKPNFDFFNYAGLH  :  178
E coli :  WQTTPPGMVITDEN---GKKKQS-YFHDFFNYAGIH  :  171
Sal    :  WQTIPPGVVTQGVN---GKKQQA-YFHDFFNYAGIH  :  171

Staph  :  RPVKIYTTPFTYVEDISVVTDFNGPTGTVEYTVDFQ  :  214
E coli :  RSVMLYTTPNTWVDDITVVTHVAQDCNHASVDWQVV  :  207
Sal    :  RSVMLYTTPKTFVEDITVVTQVADDLAQATVAWQVR  :  207

Staph  :  GKAETVKVSVVDEEGKVVASTEGLSGNVEIPNVILW  :  250
E coli :  ANGD-VSVELRDADQQVVATGQGTSGTLQVVNPHLW  :  242
Sal    :  ANGE-VRVELRDAEQQLVASGQGEKGELLLEGPRLW  :  242

Staph  :  EPLNTYLYQIKVELVNDGLTIDVYEEPFGVRTVEVN  :  286
E coli :  QPGEGYLYELCVTAKSQ-TECDIYPLRVGIRSVAVK  :  277
Sal    :  QPGEGYLYELRVIAQHQ-DEQDEYPLRVGIRSVEVK  :  277
```

FIG. 18A

09/936759

```
Staph   :  DGKFLINNKPFYFKGFGKHEDTPINGRGFNEASNVM  :  [illegible]
E coli  :  GEQFLINHKPFYFTGFGRHEDADLRGKGFDNVLMVH  :  313
Sal     :  GEQFLINHKPFYFTGFGRHEDADLRGKGFDNVLMVH  :  313

Staph   :  DFNILKWIGANSFRTAHYPYSEELMRLADREGLVVI  :  358
E coli  :  DHALMDWIGANSYRTSHYPYAEEMLDWADEHGIVVI  :  349
Sal     :  DHALMDWIGANSYRTSHYPYAEEMLDWADEHGIVII  :  349

Staph   :  DETPAVGVHLNFMATTGLGEGSERVSTWEKIR--TF  :  392
E coli  :  DETAAVGFNLSLGIGFEAGNKPKELYSEEAVNGETQ  :  385
Sal     :  DETAAVGFNLSLGISFDVGEKPKELYSDEAVNDETQ  :  385

Staph   :  EHHQDVLRELVSRDKNHPSVVMWSIANEAATEEEGA  :  428
E coli  :  QAHLQAIKELIARDKNHPSVVMWSIANEPDTRPQGA  :  421
Sal     :  RAHLQAIKELIARDKNHPSVVMWSIANEPDTRPNGA  :  421

Staph   :  YEYFKPLVELTKELDPQKRPVTIVLFVMATPETDKV  :  464
E coli  :  REYFAPLAEATRKLDP-TRPITCVNVMFCDAHTDTI  :  456
Sal     :  REYFAPLAQATRELDP-TRPITCVNVMFCDAESDTI  :  456

Staph   :  AELIDVIALNRYNGWYFDGGDLEAAKKVHEQQEFHAW  :  500
E coli  :  SDLEDVLCLNRYYGWYVQSGDLETAEKVLEKELLAW  :  492
Sal     :  TDLEDVVCLNRYYGWYVQSGDLEKAEKVLEKELLAW  :  492

Staph   :  NKRCPGKPIMITEYGADTVAGFHDIDPVMFTEEYQV  :  536
E coli  :  QEKLH-QPIIITEYGVDTLAGLHSMYTDMWSEEYQC  :  527
Sal     :  QEKLH-RPIIITEYGVDTLAGLHSMYNDMWSEEYQC  :  527

Staph   :  EYYQANHVVFDEFENPVGEQAWNFADFATSQGVMRV  :  572
E coli  :  AWLDMYHRVFDRVSAVVGEQVWNFADFATSQGILRV  :  563
Sal     :  AWLDMYHRVFDRVSAVVGEQVWNFADFATSQGIMRV  :  563
```

FIG. 18B

```
Staph     :  QGNKKGVFTRDRKPKLAAHVFRERWTNIPDFGYKN-  :  597
E coli    :  GGNKKGIFTRDRKPKSAAFLLQKRWTGM-NFGEKPQ  :  598
Sal       :  GGNKKGIFTRDRKPKSAAFLLQKRWTGM-DFGVKPQ  :  598

Staph     :  -------  :    -
E coli    :  QGGKQ--  :  603
Sal       :  QGDK---  :  602
```

FIG. 18C

```
Staph   :  ----------ATGGTAGATCTGACTAGTCTGTACCC  :  26
E.coli  :  TTATTATCTTAATGAGGAGTCCCTTATGTTACGTCC  :  36
Sal     :  ------------------------ATGTTACGTTC  :  11

Staph   :  GATCAACACCGAGACCCGTGGCGTCTTCGACCTCAA  :  62
E.coli  :  TGTAGAAACCCCAACGCGTGAAATCAAAAAACTCGA  :  72
Sal     :  TGTCGAAACCGCGACGCGAGAAATCAAAAAACTGGA  :  47

Staph   :  TGGCGTCTGGAACTTCAAGGTGGACTACGGGAAA--  :  96
E.coli  :  CGCCCTGTGGCGCATTCAGTGTGGATCGCGAAAACTG  : 108
Sal     :  CGGCCTGTGGTCGTTTTGTATGGATAGCGAAGAGTG  :  83

Staph   :  -GGACTGGAAGACAAGTGGTACGAAAGCAAGCTGAC  : 131
E.coli  :  TGGAATTCATCACGGTTCGTGGGAAAGCGCGTTACA  : 144
Sal     :  CGGCAACCCGCAGCAATGGTGGCGTCAACCGTTACC  : 119

Staph   :  CGACACTATTAGTATGCCGGTCCCAAGCAGTTACAA  : 167
E.coli  :  AGAAAGCCGGGCAATTGCTGTGCCAGGCAGTTTTAA  : 180
Sal     :  CCAAAGCCGCGCTATCGCCGTTCCGGGAAGCTATAA  : 155

Staph   :  TGACATTGGCGTGACCAAGGAAATCCCGCAACCATAT  : 203
E.coli  :  CGATCAGTTCGCCGATGCAGATATTCGTAATTATGC  : 216
Sal     :  CGATCAGTTTGCCGGTGCCGAGATCCGCAATTATGT  : 191

Staph   :  CGGATATGTCTGGTACGAACGTGAGTTCACGGTGCC  : 239
E.coli  :  GGGCAACGTCTGGTATCAGCGCGAAGTCTTTATACC  : 252
Sal     :  TGGCAACGTCTGGTATCAGCGTGAGATACGCATCCC  : 227

Staph   :  GGCCTATCTCAAGGATCAGCGTATGGTGCTCCGCTT  : 275
E.coli  :  GAAAGGTTGGGCAGGCCAGCGTATCGTGCTGCGTTT  : 288
Sal     :  GAAAGCCTGCGATCGCCAGCGCATAGTGCTGCCGTT  : 263
```

FIG. 19A

```
Staph   :  CGGCTCTGCAACTCACAAAGCAATTGTCTATGTCAA  :  ...
E.coli  :  CGATGCGGTCACTCATTACGGCAAAGTGTGGGTCAA  :  324
Sal     :  TGATGCGGTGACTCACTATGGAAAAGTTGGGTCAA  :  299

Staph   :  TGGTGAGCTGGTCGTGGAGCACAAGGGCGGATTCCT  :  347
E.coli  :  TAATCAGGAAGTGATGGAGCATCAGGGCGGCTATAC  :  360
Sal     :  TGACCAATTTTTAATGGAACATGAGGCCGCCTACAC  :  335

Staph   :  GCCATTCGAAGCGGAAATCAAGAAGTCGCTGCGTGA  :  383
E.coli  :  GCCATTTCAAGCCGATGTCACGGCGTATGTTATTGC  :  396
Sal     :  CCCGTTTGAAGCGGATATCAGCGAGCTTATCTCCGC  :  371

Staph   :  TGCCATGTAT---CGCGTCACCGTCGCGGTGGACAA  :  416
E.coli  :  GCCGAAAAGTGTACGTATCACCGTTTGTGTGAACAA  :  432
Sal     :  CGCGGAATCCGTGCGTATCACGGTATGCGTGAATAA  :  407

Staph   :  CATCCTCGACGATAGCACCCTCCCCGTCGGGCTGTA  :  452
E.coli  :  CGAACTGAACTGGCAGACTATCCCCCGCGGGCAAT-GG  :  467
Sal     :  CGAGCTGAACTGGCAGACGATCCCCCCGGGCCGT-TG  :  442

Staph   :  CAGCGAGCGCCACGAAGAGGGCCTCGCAAAAGTCAT  :  488
E.coli  :  TGATTACGCACGAAAACGG----CAAGAAAAAGCAG  :  499
Sal     :  TGACCCAGGGCGTAAACGG----TAAGAAGCAGCAA  :  474

Staph   :  TCGTAACAAGCCGAACTTCGACTTCTTCAACTATGC  :  524
E.coli  :  TCTTACTT-------CGATGATTTCTTTAACTATGC  :  528
Sal     :  GCGTATTT-------CCATGATTTCTTTAACTACGC  :  503

Staph   :  AGGCCCTGCACCGTCCGGTGAAAATCTACACGACCCC  :  560
E.coli  :  CGGGATCCATCGCAGCGTAATGCGTACACCACGCC  :  564
Sal     :  CGGTATTCATCGCAGCGTAATGCTGTACACCACGCC  :  539
```

FIG. 19B

```
Staph   :  GTTTACGTACGTCGAGGACATCTCGGTTGTGACCGA  :  596
E.coli  :  CAACACCTGGGTGGACGATATCACCGTGGTGACGCA  :  600
Sal     :  GAAAACTTTTGTGGAAGATATTACCGTCGTGACGCA  :  575

Staph   :  CTTCAATGGCCAACCCGGACTGTGCACCTATAGGGT  :  632
E.coli  :  TGTCGCGCAA--GACTGTAACCACGCGGTGTGTTGAG  :  634
Sal     :  GGTTGCTGAG--GATCTGCCTCAGGGTAGCCTGCCG  :  609

Staph   :  GGACTTTCAAGGCAAAGCCGAGACCGTGAAAGTGTC  :  668
E.coli  :  TCGCAGGTGGTGCGCCAATGCTGAT-GTCAGCGTTGA  :  669
Sal     :  TGGCAGGTACGCGCGAATGCCGAA-GTGCGTGTAGA  :  644

Staph   :  GGTCGTGGATGAGGAAGGCAAAGTGGTCGCAAGCAC  :  704
E.coli  :  ACTGCGTGATGCCGATCAACAGGTGGTTGCAAGTGG  :  705
Sal     :  GGTACGTGACGCGGAGCAACAGCTTGTCGCTTGGGG  :  680

Staph   :  CGAGGGCCTGAGCGGTAACGTGCAGATTCCGAATGT  :  740
E.coli  :  AGAAGGCACTAGCGGGACTTTGCAAGTGGTGAATCC  :  741
Sal     :  GCAAGGGGAAAAAGGTGAACTGCTGCTGGAAGGGCC  :  716

Staph   :  CATGCTCTGGGAACCACTGAACACGTATCTGTACCA  :  776
E.coli  :  GCACCTCTGGCAACCGGGTGAAGGTTATCTGTAT--  :  775
Sal     :  GCGGCTGTGGCAGCCTGCCGAGGCCTATCTTTAT--  :  750

Staph   :  GATCAAAGTGGAACTGGTGAACGCACGGACTGACCAT  :  812
E.coli  :  GAACTGTGCGTCACACGCAAAAGCCAGACAGAGTGT  :  811
Sal     :  GAACTGCGGGTCATCGCGCAGGATCAGGACGAGCAG  :  786

Staph   :  CGATGTCTATGAAGAGCCGTTCGCGGTGCGCGACCGT  :  848
E.coli  :  -GATATCTACCCGCTTCGCGTCGCGATCCGGTCAGT  :  846
Sal     :  -GATGAATATCCGCTGCGCGTCGGTATTCGCTCGGT  :  821
```

FIG. 19C

```
Staph   :  GGAAGTCAACGACGGCAAGTTCCTCATCAACAACAA  :  884
E.coli  :  GGCAGTGAAGCGCGAACAGTTCCTGATTAACCACAA  :  882
Sal     :  AGAAGTAAAACGGGAGCAGTTCCTGATCAACCATAA  :  857

Staph   :  ACCGTTCTAGTTCAAGGCCTTTGGCAAACATGAGGA  :  920
E.coli  :  ACCGTTCTAGTTTACTGCCTTTGGTCGTCATGAAGA  :  918
Sal     :  GCCTTTCTATTTCACCGGGTTCGGACGTCATGAAGA  :  893

Staph   :  CACTCCTATCAACGGCCGTCCCTTTAACGAAGCGAG  :  956
E.coli  :  TGCGGACTTACGTGGCAAAGGATTCGATAAGCTGCT  :  954
Sal     :  TGCCGATCTGCGCGGTAAGCGTTTTCATAACGTGCT  :  929

Staph   :  CAATGTGATGGATTTCAATATCCTCAAATGGATCGG  :  992
E.coli  :  GATGGTGCAGGACCACGCATTAATGGACTGGATTGG  :  990
Sal     :  GATGGTGCAGGACCACGCGCTAATGGACTCGATCGG  :  965

Staph   :  CGCGAACAGGTTCCGGACCGCACACTATCCGTACTC  : 1028
E.coli  :  GGCGAACTCGTACCGTACCTCGCATTACCCTTACGC  : 1026
Sal     :  TGCGAACTCTTACCGTACCTCGCATTACCCTTATGC  : 1001

Staph   :  TGAAGAGTTGATGCGTCTTCCGGATCGCGAGGGTCT  : 1064
E.coli  :  TGAAGAGATGGTCGACTGGCCAGATGAAGATGCCAT  : 1062
Sal     :  CGAAGAGATGGTCGACTGGGCGGACGAACATGGCAT  : 1037

Staph   :  GGTCGTGATCGACGAGACTCCGGCAGTTGCGGTGCA  : 1100
E.coli  :  CGTCGTCATTGATGAAACTGCTGCTGTCGGCTTTAA  : 1098
Sal     :  CGTGATCATTGATGAAACGGCCGCCGTGCGATTCAA  : 1073

Staph   :  CCTCAACTTCATCGCCACCACGGGACTCGGCGAAGG  : 1136
E.coli  :  CCTCTCTTTAGGCATTGGTTTCGAAGCGGCCAACAA  : 1134
Sal     :  CCTGTCTTTAGGGATTAGCTTTCATGTCGGCGAAAA  : 1109
```

FIG. 19D

```
Staph   :  ---GAGCGAGCGCGTCAGTACCTGGGAGAAGATTCG  : 1199
E.coli  :  GCCGAAACAACTGTACAGCGAAGAGGCAGTCAACGG  : 1170
Sal     :  ACCCAAAGAGCTCTACAGCGATGAGGCCGTGAACGA  : 1145

Staph   :  GACGTTTGAGCAC---CATCAAGACGTTCTCCGTGA  : 1202
E.coli  :  GGAAACTCAGCAAGCGCAGTTAGAGCGGATTAAAGA  : 1206
Sal     :  TGAAACGCAGCGCGCGCAGCTGCAGGCAATTAAGGA  : 1181

Staph   :  ACTGGTGTCTCCTGAGAAGAACCATCCAAGCGTCGT  : 1238
E.coli  :  GCTGATAGCGCCTGACAAAAACCAGCCAAGCGTGGT  : 1242
Sal     :  GCTCATTGCCCCCGATAAGAACCAGCCAAGCGTCGT  : 1217

Staph   :  CATGTGGAGCATCGCCAACGAGGCGGCGACTGAGGA  : 1274
E.coli  :  CATGTGGAGTATTGCCAACGAACCGGATACCCGTCC  : 1278
Sal     :  CATGTGGAGTATCGCCAACGAACCGGATACCCGCCC  : 1253

Staph   :  AGAGGGCGCGTAGGAGTAGTTCAAGCCCTTGGTCGA  : 1310
E.coli  :  CCA-AGTGCACGGAATATTTCG--CCACTGCCGGA  : 1311
Sal     :  GAACGGCGCGCGCGAATAGTTCGCTCCGCTGGCGCA  : 1289

Staph   :  GCTGACCAAGGAACTCGACCCACAGAAGCGTCCGGT  : 1346
E.coli  :  AGGAACGCGTAAACTCGACCC---GACGCGTCCGAT  : 1344
Sal     :  GGCAACGCGCGAACTCGATCC---TACACGTCCGAT  : 1322

Staph   :  CACGATCGTGCTGTTTGTCATGGCTACCCCGGAGAC  : 1382
E.coli  :  CACCTGCGTCAATGTAATGTTCTGCGACGCTCACAC  : 1380
Sal     :  AACCTGCGTGAACGTGATGTTCTGCGATGCGGAAAG  : 1358

Staph   :  GGACAAAGTCGCCGAACTGATTGACGTCATCGCGCT  : 1418
E.coli  :  CGATACCATCAGCGATCTCTTTGATGTGCTGTGCCT  : 1416
Sal     :  CGAGACCATTACCGATCTCTTTGATGTCGTTTGCCT  : 1394
```

FIG. 19E

```
Staph   :  CAATCGCTATAACGGATGGTACTTGCATGGCGGTGA  : 1454
E.coli  :  GAACCGTTATTACGGATGGTATGTCCAAAGCGGCGA  : 1450
Sal     :  GAACCGCTACTACGGCTCGTATGTACAAAGCGGCGA  : 1430

Staph   :  TCTCGAAGCGGCCAAAGTCCATCTCCGCCAGGAATT  : 1490
E.coli  :  TTTCGAAACGGCAGACAAGGTACTGGAAAAAGAAGT  : 1488
Sal     :  TCTGGAGAAGGCTGAGAAAGTGCTGGAGTAAGAGCT  : 1466

Staph   :  TCACGCGTGGAACAAGCGTTGCCCAGGAAAGCCGAT  : 1526
E.coli  :  TCTGGCCTGGCAGGAGAAAGTGC---ATGAGCCGAT  : 1521
Sal     :  TCTGGCCGTGGCAGGAGAAAGTGC---ACGGCCCGAT  : 1499

Staph   :  CATGATCACTGAGTACGCCGCAGACACCGTTGCGGC  : 1562
E.coli  :  TATCATCACGGAATACGGCGTGGATACGTTAGGCGG  : 1557
Sal     :  TATCATCACCGAATACGGCGTCGATACGCTTGCAGG  : 1535

Staph   :  CTTTCACGACATTGATCCAGTGATGTTCACCGAGCA  : 1598
E.coli  :  GCTGCACTCAATGTACACGGACATGTGGAGTGAAGA  : 1593
Sal     :  CCTGCATTCCATGTACAACGATATGTGGAGCGAAGA  : 1571

Staph   :  ATATCAAGTCGAGTACTACCAGGCGAAGCACGTCGT  : 1634
E.coli  :  GTATCAGTCTGCATGGCTGGATATGTATCACCGCGT  : 1629
Sal     :  GTACCAGTGCGCCTGGCTTCATATGTACCATCGCGT  : 1607

Staph   :  GTTCGATGAGTTTGAGAACTTCGTGGGTGAGCAAGC  : 1670
E.coli  :  CTTTGATCCGCGTCAGCGCCGTCGTCGGTGAACAGGT  : 1665
Sal     :  GTTTGATCGCGTCAGCGGCGTCGTCGGCGAGCAGGT  : 1643

Staph   :  GTGGAACTTCGCGGACTTCGCGACCTCTCAGGGCGT  : 1706
E.coli  :  ATGGAATTTCGCCGATTTTGCGACCTCGCAAGGCAT  : 1701
Sal     :  ATGGAACTTCGCCGACTTGGCCACTTCGCAGGGCAT  : 1679
```

FIG. 19F

Figure 19G

```
Staph     :  GATGCGCGTCCAAGCAAACAAGAAGCGCGTGTTCAC  : 1742
E.coli    :  ATTGCGCGTTGGCGGTAACAAGAAACGGATGTTCAC  : 1737
Sal       :  TATGCGCGTTGGCGGCAACAAAAAAGGTATATTCAC  : 1715

Staph     :  TCGTGACCGCAAGCCGAAGCTCGCCGCGCACGTCTT  : 1778
E.coli    :  TCGCGACCGCAAACCGAAGTCGGCGGCTTTTCTGCT  : 1773
Sal       :  CCGCGACAGAAAACCAAAATCGGCGGCCTTCCTGCT  : 1751

Staph     :  TCGCGAGCGCTGGACCAACATTCCAGATTTCGCGCTA  : 1814
E.coli    :  GCAAAAACGCCTGGACTGGCAT---GAACTTCGGTGA  : 1806
Sal       :  GCAAAAACGCTGGACCGGCAT---GGACTTTGGCGT  : 1784

Staph     :  CAAGAAG------------------------------  : 1821
E.coli    :  AAAACGGCAGCAGGGAGGCAAACAATGAATCAACAA  : 1842
Sal       :  GAAGCCCCAGCAGGGAGATAAATAATGA--------  : 1812

Staph     :  ------------------------------------  :    -
E.coli    :  CTCTCCTGGCGCACCATCGTCGGCTACAGCCTCGGT  : 1878
Sal       :  ------------------------------------  :    -

Staph     :  ------------------------------------  :    -
E.coli    :  GACGTCGCCAATAACTTCGCCTTCGCAATGGGGGCG  : 1914
Sal       :  ------------------------------------  :    -

Staph     :  ------------------------------------  :    -
E.coli    :  CTCTTCCTGTTGAGTTACTACACCGACGTCGCTGGC  : 1950
Sal       :  ------------------------------------  :    -

Staph     :  ------------------------------  :    -
E.coli    :  GTCGGTGCCGCTGCGGCGGGCACCATGCTG  : 1980
Sal       :  ------------------------------  :    -
```

FIG. 19G